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OM protein - protein search, using sw model

Run on: December 20, 2002, 16:20:40 ; Search time 17 Seconds
(without alignments)
3688.953 Million cell updates/sec

Title: US-09-697-898-2
Perfect score: 7825
Sequence: 1 MAAAGNRASSGFFGARAT.....PQDRPPSRELLKHPVFTTW 1512

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	7515	96.0	1495	M3K1_HUMAN	Q12333 homo sapien
2	6920.5	88.4	1493	M3K1_MOUSE	P53349 mus musculus
3	6892.5	88.1	1493	M3K1_RAT	Q62925 rattus norv
4	619	7.9	1478	BCK1_YEAST	Q01389 saccharomyc
5	559	7.1	626	M3K3_MOUSE	Q61084 mus musculus
6	558.5	7.1	626	M3K3_HUMAN	Q99759 homo sapien
7	543.5	6.9	659	BYR2_SCHPO	P28829 schizosacch
8	536.5	6.9	618	M3K2_HUMAN	Q9Y205 homo sapien
9	535	6.8	738	STI1_YEAST	P23561 saccharomyc
10	531	6.8	619	M3K2_MOUSE	Q61083 mus musculus
11	517.5	6.6	1116	MKHL_SCHPO	Q10407 schizosacch
12	502.5	6.4	1607	M3K4_HUMAN	Q9Y614 homo sapien
13	475	6.1	1597	M3K4_MOUSE	O08648 mus musculus
14	433.5	5.5	1401	WIS4_SCHPO	O4299 schizosacch
15	430.5	5.5	1374	M3K5_HUMAN	Q99683 homo sapien
16	429.5	5.5	1379	M3K5_MOUSE	Q35099 mus musculus
17	423	5.4	1579	SSK2_YEAST	P53599 saccharomyc
18	410	5.2	1436	WTN1_SCHPO	O74304 schizosacch
19	408.5	5.2	1011	M3K6_HUMAN	O95382 homo sapien
20	398.5	5.1	658	PAK1_SCHPO	P50527 schizosacch
21	386.5	5.0	939	ST20_YEAST	Q03497 saccharomyc
22	387.5	5.0	544	PAK3_HUMAN	O75914 homo sapien
23	379	4.8	545	PAK1_MOUSE	O88643 mus musculus
24	378.5	4.8	524	PAK3_RABIT	Q29502 oryctolagus
25	377.5	4.8	544	PAK2_HUMAN	Q62829 rattus norv
26	377.5	4.8	545	PAK1_HUMAN	Q13153 homo sapien
27	377	4.8	544	PAK1_RAT	P35465 rattus norv
28	375.5	4.8	426	ST25_MOUSE	Q03201 mus musculus
29	374.5	4.8	524	PAK2_HUMAN	Q31177 homo sapien
30	373.5	4.8	1062	PAK2_SCHPO	P41892 schizosacch
31	373.5	4.8	1230	CA2_CANAL	Q92212 candida alb
32	371	4.7	942	M3KE_MOUSE	Q9W16 mus musculus
33	370.5	4.7	426	ST25_HUMAN	O00506 homo sapien

34	367.5	4.7	524	1	PAK2_RAT	Q64303 rattus norv
35	366.5	4.7	544	1	PAK3_MOUSE	Q61036 mus musculus
36	364	4.7	443	1	ST24_HUMAN	O9Y60 homo sapien
37	360.5	4.6	288	1	PEF1_SCHPO	O74456 schizosacch
38	360	4.6	646	1	CNK_HUMAN	Q9H464 homo sapien
39	359.5	4.6	631	1	CNK_MOUSE	Q50806 mus musculus
40	359.5	4.6	1314	1	SS22_YEAST	P53900 saccharomyc
41	355	4.5	947	1	M3KE_HUMAN	O99558 homo sapien
42	352.5	4.5	384	1	ARK1_SCHPO	O59790 schizosacch
43	352	4.5	615	1	CNK_RAT	Q9T011 rattus norv
44	350	4.5	1914	1	KMLS_HUMAN	Q15746 homo sapien
45	347	4.4	974	1	CC15_YEAST	P27636 saccharomyc

ALIGNMENTS

RESULT 1
M3K1_HUMAN
ID M3K1_HUMAN STANDARD; PRT: 1495 AA.
AC Q13233;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mitogen-activated protein kinase kinase kinase 1 (EC 2.7.1.1-)
DE (MAPK/ERK kinase kinase 1) (MEK kinase 1) (MEKK 1) (Fragment).
GN MAP3K1 OR MAPKKK1 OR MEKK1 OR MEKK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99026111; PubMed=9808624;
RA Xia Y., Wu Z., Su B., Murray B., Karin M.;
RT "JNK1 organizes a MAP kinase module through specific and sequential
RT interactions with upstream and downstream components mediated by its
RT amino-terminal extension."
RL Genes Dev. 12:3369-3381(1998).
RN [2]
RP SEQUENCE OF 1221-1257 FROM N.A.
RC TISSUE=Leukocyte;
RX MEDLINE=96169565; PubMed=8597633;
RA Vinik B.S., Kay E.S., Fiedorek F.T.;
RT "Mapping of the MEK kinase gene (MeKk) to mouse chromosome 13 and
RT human chromosome 5."
RL Mamm. Genome 6:782-783(1995).
CC -1- FUNCTION: CAN PHOSPHORYLATE AND ACTIVATE MAPK1 AND MAPK2
CC (MEK1/MEK2) WHICH LEADS TO PHOSPHORYLATION OF MAP KINASES. IT IS
CC ALSO A HIGHLY EFFICIENT ACTIVATOR OF THE JNK CASCADE.
CC -1- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC
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CC
CC EMBL; AF042838; AAC97073.1; -
CC EMBL; U29671; AAB05828.1; -
CC HSSP; Q00534; 1BI7.
CC SWISS-2DPAGE; Q13233; HUMAN.
CC Genew; HGNC:6848; MAP3K1.
CC MIM; 600982; -
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC InterPro; IPR001841; Znf_ring.
CC Pfam; PF00069; pkinase; 1.

DR	ProdDom: PD000001; Euk_pkinase; 1.	
DR	SMART: SM00184; RING; 1.	
DR	SMART: SM00220; S.TK; 1.	
DR	PROSITE: PS00107; PROTEIN KINASE ATP; 1.	
DR	PROSITE: PS00101; PROTEIN KINASE_DOM; 1.	
DR	PROSITE: PS00108; PROTEIN KINASE_ST; 1.	
DR	PROSITE: PS00518; ZF_RING_1; FALSE_NEG.	
DR	PROSITE: PS00089; ZF_RING_2; 1.	
KW	Transferase; Serine/threonine-protein kinase; ATP-binding;	
KW	Phosphorylation; zinc-finger.	
FT	NON_TER 1 1	
FT	2N_FING 424 473	RING-TYPE
FT	DOMAIN 1226 1491	PROTEIN KINASE
FT	DOMAIN 403 412	POLY-SER.
FT	DOMAIN 925 932	POLY-THR.
FT	DOMAIN 1165 1170	POLY-GLU.
FT	NP_BIND 1232 1239	ATP (BY SIMILARITY).
FT	BINDING 1255 1255	ATP (BY SIMILARITY).
FT	ACT_SITE 1352 1352	BY SIMILARITY
SQ	SEQUENCE 1495 AA; 2D6E6B52E7AFC4B CRC64;	
Query Match 96.0%; Score 7515; DB 1; Length 1495;		
Best Local Similarity 97.8%; Pred. No. 1.2e-308;		
Matches 1461; Conservative 3; Mismatches 28; Indels 2; Gaps 2;		
QY	21	SPEAGGGGALKASSAPAAAGLLREAGSGRGRADRRRLKRVSVLDDLPQPLFL 80
DB	2	SPEAGGGGALKASSAPAAAGLLREAGSGRGRADRRRLKRVSVLDDLPQPLFL 61
QY	81	AASPPASSTSPSPADAAAGSGTGFPVAVPPPHGAAARGCAHLTESVAAPDSCAGSPAA 140
DB	62	AASPPASSTSPSPADAAAGSGTGFPVAVPPPHGAAARGCAHLTESVAAPDSCAGSPAA 121
QY	141	AEPCEKAPAAEPSAPAAAGREKENETLGLKHKMDRDEERWIREKATCAMPWKHE 200
DB	122	AEPCEKAPAAEPSAPAAAGREKENETLGLKHKMDRDEERWIREKATCAMPWKHE 181
QY	201	WLERNRGPPVVKPIPVKGDGSEMHAAEAGEVOASAASPAKGRRRSPGNSPSGR 260
DB	182	WLERNRGPPVVKPIPVKGDGSEMHAAEAGEVOASAASPAKGRRRSPGNSPSGR 241
QY	261	TVKSESGVRRKRVSPVFGSGRTTPRRAPSPDGFSPYSPETNRVNVKVMARLYLQ 320
DB	242	TVKSESGVRRKRVSPVFGSGRTTPRRAPSPDGFSPYSPETNRVNVKVMARLYLQ 301
QY	321	QIGPNSFLIGDSDPNKYRVFIPGQNCSCARGTFCIHLLFVMLRVFOLESDPMLARKTL 380
DB	302	QIGPNSFLIGDSDPNKYRVFIPGQNCSCARGTFCIHLLFVMLRVFOLESDPMLARKTL 361
QY	381	KNFVESLFOKYHRRSRKAPSRNTIQFVSRMSNHLSSSTSTSSSENSIKDEE 440
DB	362	KNFVESLFOKYHRRSRKAPSRNTIQFVSRMSNHLSSSTSTSSSENSIKDEE 421
QY	441	QMCPICLLGLMDESLTVCEGDCRNKLHHCMSIWAECRRNREPLICLCRSKWRSHDF 500
DB	422	QMCPICLLGLMDESLTVCEGDCRNKLHHCMSIWAECRRNREPLICLCRSKWRSHDF 481
QY	501	YSHELSPVSPSSLRAAQOQTVOOQPLAGSRNQNENFNTHYGTQOIPPAYKDIAEPW 560
DB	482	YSHELSPVSPSSLRAAQOQTVOOQPLAGSRNQNENFNTHYGTQOIPPAYKDIAEPW 541
QY	561	IQVFGMELVGLCFRRNNVREMLRLSHDVSQALLANGESTGNSGSGSGSPGGATS 620
DB	542	IQVFGMELVGLCFRRNNVREMLRLSHDVSQALLANGESTGNSGSGSGSPGGATS 601
QY	621	GSSQTSISGDVVEACCSVLMSVCAADPVYKVVAAKTLRLAMLYVTPCHSIAERIKLQRL 680
DB	602	GSSQTSISGDVVEACCSVLMSVCAADPVYKVVAAKTLRLAMLYVTPCHSIAERIKLQRL 661
QY	681	QPVYDTILVKADANSRTSLSISLLELCKGQAGELAVGREILKAGSIGIGGVYVYVLC 740
DB	662	QPVYDTILVKADANSRTSLSISLLELCKGQAGELAVGREILKAGSIGIGGVYVYVLC 721

QY	741	ILGNQTESNNWOELLGRCLIDRLLEFPAEPHYPHIVSDVSQAEPVEIRYKKLLSLTF 800
DB	722	ILGNQTESNNWOELLGRCLIDRLLEFPAEPHYPHIVSDVSQAEPVEIRYKKLLSLTF 781
QY	801	ALQSDNHSMTYKGLSRRIYLLSSARMTTPVHVSFKLLEMLSVSS-STHFFRRRLMAI 859
DB	782	ALQSDNHSMTYKGLSRRIYLLSSARMTTPVHVSFKLLEMLSVSS-STHFFRRRLMAI 841
QY	860	ADEVEIAEAIQLGVEDTLDGQQ-DSFLQASVNNYLETENSSSPECTVHLEKTIGKGLCAT 918
DB	842	ADEVEIAEAIQLGVEDTLDGQQ-DSFLQASVNNYLETENSSSPECTVHLEKTIGKGLCAT 901
QY	919	KLSASEDISERLASISVGPSSSTTTTTTTEQPKPMVQTKGRPHSQCLNSPLSHHSQL 978
DB	902	KLSASEDISERLASISVGPSSSTTTTTTTEQPKPMVQTKGRPHSQCLNSPLSHHSQL 961
QY	979	MPALSTPSSSTSPVPAGTATDVSKHRLQGFPCIPASQTPQTKFSLQFHRNCPENKD 1038
DB	962	MPALSTPSSSTSPVPAGTATDVSKHRLQGFPCIPASQTPQTKFSLQFHRNCPENKD 1021
QY	1039	SKLSPVFTQSRPLPSSNTHRPKPSRPTPGNTSKGDPKSNMTLDLNSSSKCDSDSFGCS 1098
DB	1022	SKLSPVFTQSRPLPSSNTHRPKPSRPTPGNTSKGDPKSNMTLDLNSSSKCDSDSFGCS 1081
QY	1099	SNSSNAVIPSDETFTVPEEKCRCLDVNTLNSSIEDLLEASMPSSDTTVPKSEVAVLSP 1158
DB	1082	SNSSNAVIPSDETFTVPEEKCRCLDVNTLNSSIEDLLEASMPSSDTTVPKSEVAVLSP 1141
QY	1159	EKAENDTYKDDVNNHKKCKEKEAEPEEALAIAMAMASQDALPIVPOLOVENGEDIII 1218
DB	1142	EKAENDTYKDDVNNHKKCKEKEAEPEEALAIAMAMASQDALPIVPOLOVENGEDIII 1201
QY	1219	IQDTPETLPGHTKAKQPYREDTEWLKGOQIGLGFSSCYQADVGTLMAVKQVTVYR 1278
DB	1202	IQDTPETLPGHTKAKQPYREDTEWLKGOQIGLGFSSCYQADVGTLMAVKQVTVYR 1261
QY	1279	NTSSEQEEVVEALREIRRMHSHLNHPNIIIRMLGATCEKSNYNLFIEWAGGSVAHLISKY 1338
DB	1262	NTSSEQEEVVEALREIRRMHSHLNHPNIIIRMLGATCEKSNYNLFIEWAGGSVAHLISKY 1321
QY	1339	GAFKESVWVINYTEOLLRGLSYLHENOIIHRDVKGANLLIDSTGQRLIADFGAARLASK 1398
DB	1322	GAFKESVWVINYTEOLLRGLSYLHENOIIHRDVKGANLLIDSTGQRLIADFGAARLASK 1381
QY	1399	GTGAGFQGLLGTIAFMAPEVLRGQYGRSCDVMSVGCATTEMACAKPPWNAEKHSNHL 1458
DB	1382	GTGAGFQGLLGTIAFMAPEVLRGQYGRSCDVMSVGCATTEMACAKPPWNAEKHSNHL 1441
QY	1459	ALIFKTASATTAPSPHSLSPGLRDVALCLELOQDPPSRELLKHPVFTTW 1512
DB	1442	ALIFKTASATTAPSPHSLSPGLRDVALCLELOQDPPSRELLKHPVFTTW 1495

RESULT 2
M3K1_MOUSE
ID M3K1_MOUSE STANDARD: PRT; 1493 AA.
AC P53349; Q60831; Q9R256; Q9R0U3;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mitogen-activated protein kinase kinase 1 (EC 2.7.1.-)
DE (MAPK/ERK kinase kinase 1) (MEK kinase 1) (MEKK 1).
GN MAP3K1 OR MEKK1 OR MEKK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Lange C.A., Blumer K.J., Sather S.L., Johnson G.L.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-659 FROM N.A.

RC TISSUE=Spleen;
RX MEDLINE=99455010; PubMed=10523642;
RA Ito M., Yoshioke K., Akechi M., Yamashita S., Takamatsu N.,
RA Sugiyama K., Hibi M., Nakabeppu Y., Shiba T., Yamamoto K.-I.,
RT "JSAPI, a novel Jun N-terminal protein kinase (JNK)-binding protein
that functions as a scaffold factor in the JNK signaling pathway.";
RL Mol. Cell. Biol. 19:7539-7548(1999).
RN [3]
RP SEQUENCE OF 660-1493 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=93227040; PubMed=8385802;
RA Lange-Carter C.A., Pleiman C.M., Gardner A.M., Blumer K.J.,
RA Johnson G.L.,
RT "A divergence in the MAP kinase regulatory network defined by MEK
kinase and Raf.";
RL Science 260:315-319(1993).
RN [4]
RP SEQUENCE OF 796-1493 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Heart;
RA Whitmarsh A.J., Shore P., Sharrocks A.D., Davis R.J.,
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CAN PHOSPHORYLATE AND ACTIVATE MAPKK 1 AND MAPKK 2
(MEK1/MEK2) WHICH LEADS TO PHOSPHORYLATION OF MAP KINASES.
CC POTENTIALLY ACTIVATES THE JNK/SAPK GROUP OF MAP KINASES.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE HEART AND SPLEEN WHILE
CC A LOWER LEVEL EXPRESSION IS SEEN IN THE LIVER.
CC -!- PTM: AUTOPHOSPHORYLATED.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC
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CC
CC EMBL; AF117340; AAD25049.1; -;
DR EMBL; AB014614; BAA85878.1; -;
DR EMBL; L13103; AAA97500.1; ALT_INIT.
DR EMBL; U23470; AAA85038.1; -;
DR HSSP; Q00534; 1B17.
DR MGD; MGI:1346672; Map3k1.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF000184; Znf_ring.
DR Pfam; PF000069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Transpherase: Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Zinc-finger.
FT ZN_FING 436 487 RING-TYPE.
FT DOMAIN 1224 1489 PROTEIN KINASE.
FT DOMAIN 25 32 POLY-GLY.
FT DOMAIN 74 149 PRO-RICH.
FT DOMAIN 233 291 PRO-RICH.
FT DOMAIN 417 426 POLY-SER.
FT NP_BIND 1230 1237 ATP (BY SIMILARITY).
FT BINDING 1233 1253 ATP (BY SIMILARITY).
FT ACT_SITE 1350 1350 BY SIMILARITY.
FT CONFLICT 30 39 GGAQQSGA -> AQQSG (IN REF. 2).
FT CONFLICT 103 103 MISSING (IN REF. 2).
FT CONFLICT 257 257 V -> E (IN REF. 2).

FT	CONFLICT	307	307	M -> V (IN REF. 2).
FT	CONFLICT	413	413	S -> C (IN REF. 2).
FT	CONFLICT	559	559	V -> A (IN REF. 2).
FT	CONFLICT	883	883	V -> L (IN REF. 3).
FT	CONFLICT	1467	1467	V -> L (IN REF. 3).
SQ	SEQUENCE	1493	AA; 161288	MW; CA65C9B7703C6BF9 CRC64;
Query Match				
Best Local Similarity 89.6%; Pred. No. 1.1e-283;				
Matches 1360; Conservative 46; Mismatches 81; Indels 31; Gaps 11;				
QY	1	MAAAGNRASSSGFFGATATSP	EA---GGGGGALKASSAPAA--AAGLLRACSGGGERAD	56
DB	1	MAAAGNRASSSGFFGATATSP	EA---GGGGGALKASSAPAA--AAGLLRACSGGGERAD	60
QY	57	WRRQLRKVRSELDQLEQLEL	-AASPPASSTSPSPADAAAGSGTGFQPVAVPPPHG	115
DB	61	WRRQLRKVRSELDQLEQLEL	-AASPPASSTSPSPADAAAGSGTGFQPVAVPPPHG	120
QY	116	AASGGGAHLTESVAAPDSG	ASSPAAAPGEGKRAPAEPSAPAAAPAGREMKETLKLGHK	175
DB	121	AASCGSHSALAARSDGARS	FAGAEPP-----PS-AAAPSGREMKETLKLGHK	170
QY	176	MDDPERMIREKLKATCM	PAWKHELRNRGPPVVKPIPVKGDGSENMHAAESPGE	235
DB	171	MDDPERMIREKLKATCM	PAWKHELRNRGPPVVKPIPVKGDGSENMHAAESPGE	230
QY	236	VQASAASPASKRRSPSGNS	SGRTVYKSPSGVRRKRVPVPFQSGRITPPRRAPSPDG	295
DB	231	QAGSAAPAPKRRSPSGNS	SGRSVKPESPGVRRKRVPVPFQSGRITPPRRAPSPDG	290
QY	296	FSPYSPETRRVNRVNR	ARLYLLOQIGNSFLIGGSDPNKYRVFTGPNCCSCARCTFC	355
DB	291	FSPYSPETRRVNRVNR	ARLYLLOQIGNSFLIGGSDPNKYRVFTGPNCCSCARCTFC	350
QY	356	IHLFVNLVRFQLEPSP	MLWRKTLKNFEVESLFQKYHRSRRSRIKAPSRNTIQFVSRM	415
DB	351	IHLFVNLVRFQLEPSP	MLWRKTLKNFEVESLFQKYHRSRRSRIKAPSRNTIQFVSRM	410
QY	416	SNSTLSSSTSTSSSEN	SKDEEQMCPCLLGMLEDESLTVCEDCGRKLHHCMSIW	475
DB	411	SNSTLSSSTSTSSSEN	SKDEEQMCPCLLGMLEDESLTVCEDCGRKLHHCMSIW	470
QY	476	AEECRNRREPLICLCR	SKWRSHDFYSHELSPPVDSPLRAAQOQTVQOQPLAGS--RRN	534
DB	471	AEECRNRREPLICLCR	SKWRSHDFYSHELSPPVDSPLRAAQOQTVQOQPLAGS--RRN	530
QY	535	QESFNLTHTYGTQOIP	PAYKDIAEPNIOVFCMELVGLFSRNNVNRRLRLSHDVSGA	594
DB	531	QESFNLTHTYGTQOIP	SAYKDIAEPNIOVFCMELVGLFSRNNVNRRLRLSHDVSGA	590
QY	595	LLLANGESTGNSGGSG	SGSGATSGSSQTSISGDVVEACCSVLMSVCADPVYKVYVAA	654
DB	591	LLLANGESTGNSGGSG	SGSGSLSAGASGSSQPSISGDVVEACCSVLMSVCADPVYKVYVAA	650
QY	655	LKTRAMLVYTPCHSLA	ERIKQLRLQPVVDITLVKCADANSRTSLSITLLECKGQA	714
DB	651	LKTRAMLVYTPCHSLA	ERIKQLRLQPVVDITLVKCADANSRTSLSITLLECKGQA	710
QY	715	GELAVGREILKAGSIG	IGGVYVNLNCGNOTESNNQELGLCLIDRLLEFPAPFYP	774
DB	711	GELAVGREILKAGSIG	IGGVYVNLNCGNOTESNNQELGLCLIDRLLEFPAPFYP	770
QY	775	HIVSTDVSAQPEVIRY	KKLLSLTTFALQSDNSHSMVGKLSRIYIYSSARMTVTPHVF	834
DB	771	HIVSTDVSAQPEVIRY	KKLLSLTTFALQSDNSHSMVGKLSRIYIYSSARMTVTPHVF	830
QY	835	SKLLMLSVSSSTHFT	RRMRRLMAIDEVEIAEAQLQVEDTLDGQDSFLOQASVNNYL	894
DB	831	SKLVTMLNAGSTHFT	RRMRRLMAIDEVEIAEAQLQVEDTLDGQDSFLOQASVNNYL	889
QY	895	ETTENSPECTVHLEK	TGKGCATKLSASSEDISERLASISVGPSSSTTTTTTTEQPKP	954

Db 890 ---ENSSLEHTVHREKTKGSLATRLSSSEDI8DRLAGVSVGLPSS-----TTTEQPKP 941
QY 955 MYOTGRPHSQCINSLSHSOLMFPAALSPSSSTPSVPAAGTADYSKHLRQGFICRI 1014
Db 942 AVQTKGRPHSQCINSLSPHS-HAQLMFPAPSAFCSAPSVP-----DISKHPQAFVCKI 995
QY 1015 PASPQTKRKSLOPHRCNPKNSDKLSPLVFTOSRPLPSSNIHRPAPSRPTDNTSKQG 1074
Db 996 PASPQTKRKSLOPHRCNPKNSDKLSPLVFTOSRPLPSSNIHRPAPSRPTDNTSKLG 1055
QY 1075 DRKSNMFLDLNSSLKCDSDSFCSSNSNNAVIPSDETFTVPEEKCRDVTNELNSSTED 1134
Db 1056 DATKSSMFLDLGASRCDDSDSGGNGSNNAVIPSDETFTVPEEKCRDVTNELNSSTED 1115
QY 1135 LLEASNPSSDTTFTKSEVAVLSPEKAENDDTYKDDVHNOKCKEKKAEAEALAIAMA 1194
Db 1116 LLEASNPSSDTTFTKSEVAVLSPEKAENDDTYKDDVHNOKCKEKKAEAEALAIAMA 1175
QY 1195 MASQDALPIVQLOVENGEDIIIIQQDTPTLPQHTKAKOPYREDTEWLKGOQIGLGF 1254
Db 1176 MASQDALPIVQLOVENGEDIIIIQQDTPTLPQHTKAKOPYREDTEWLKGOQIGLGF 1235
QY 1255 SSCYQAQDVGTGLMAVKQVTVYRNTSEQEVEVLEALREIRNMSHLNHPNIRMLGATC 1314
Db 1236 SSCYQAQDVGTGLMAVKQVTVYRNTSEQEVEVLEALREIRNMSHLNHPNIRMLGATC 1295
QY 1315 EKSNNLFTFWAGGSVAHLLSKYGAFFESVYVINTTEQLRGLSYLHENOIIHRDVKGAN 1374
Db 1296 EKSNNLFTFWAGGSVAHLLSKYGAFFESVYVINTTEQLRGLSYLHENOIIHRDVKGAN 1355
QY 1375 LLTSDTGRLRIADFGAARLASKGTGAGEFQGLLGTIAFMAPEVLGRQOYGRSCDVMS 1434
Db 1356 LLTSDTGRLRIADFGAARLASKGTGAGEFQGLLGTIAFMAPEVLGRQOYGRSCDVMS 1415
QY 1435 VCAIITEMACAPPPNAEKSHLALIFKIASATTAPSPSHLSPLGRDVALRCLELOPQ 1494
Db 1416 VCAIITEMACAPPPNAEKSHLALIFKIASATTAPSPSHLSPLGRDVALRCLELOPQ 1475
QY 1495 DRPPSRELLKHPVFRFTW 1512
Db 1476 DRPPSRELLKHPVFRFTW 1493

RESULT 3
M3K1_RAT STANDARD; PRT; 1493 AA.
ID AC Q62925;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mitogen-activated protein kinase kinase 1 (EC 2.7.1.-)
GN MAP3K1 OR MEK1 OR MEKK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS.
RC TISSUE=Brain;
RX MEDLINE=96224276; PubMed=8643568;
RA Xu S., Robbins D.J., Christerson L.B., English J.M.,
RA Vanderbilt C.A., Cobb M.H.;
RT "Cloning of rat MEK kinase 1 cDNA reveals an endogenous membrane-
associated 195-kDa protein with a large regulatory domain";
RL Proc. Natl. Acad. Sci. U.S.A. 93:5291-5295(1996).
CC -!- FUNCTION: CAN PHOSPHORYLATE AND ACTIVATE MAPKK 1 AND MAPKK 2
CC (MEK1/MEK2) WHICH LEADS TO PHOSPHORYLATION OF MAP KINASES. MOST
CC POTENTIALLY ACTIVATES THE JNK/SAPK GROUP OF MAP KINASES, AND LESS
CC EFFICIENTLY ERK2 OR p38.
CC -!- SUBCELLULAR LOCATION: MEMBRANE ASSOCIATED.
CC -!- TISSUE SPECIFICITY: MOST HIGHLY EXPRESSED IN SPLEEN, KIDNEY, AND
CC LUNG.

CC -!- PTM: AUTOPHOSPHORYLATED.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to a license@isb-sib.ch).
CC
CC -----
CC EMBL; U48596; AAC52596.1; --
CC HSP; Q00534; I317;
CC InterPro: IPR000719; Euk_pkinase.
CC InterPro: IPR002290; Ser_thr_pkinase.
CC InterPro: IPR001841; Znf_ring.
CC Pfam: PF00069; pkinase; 1.
CC ProDom: PD000001; Euk_pkinase; 1.
CC SMART; SM00184; RING; 1.
CC SMART; SM00220; S_TKC; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
CC PROSITE; PS00089; ZF_RING_2; 1.
CC Transfaser: Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Zinc-finger.
KW
FT ZN_FING 433 482 RING-TYPE.
FT DOMAIN 1224 1489 PROTEIN KINASE.
FT DOMAIN 25 29 POLY-GLY.
FT DOMAIN 74 149 PRO-RICH.
FT DOMAIN 233 291 PRO-RICH.
FT DOMAIN 412 421 POLY-SER.
FT DOMAIN 1163 1168 POLY-GLU.
FT NP_BIND 1230 1237 ATP (BY SIMILARITY).
FT BINDING 1253 1253 ATP (BY SIMILARITY).
FT ACT_SITE 1350 1350 BY SIMILARITY.
FT MUTAGEN 1369 1369 D->A; INACTIVATION.
SQ SEQUENCE 1493 AA; 161315 MW; 8C5F29F866898524 CRC64;

Query Match 88.1%; Score 6892.5; DB 1; Length 1493;
Best Local Similarity 89.2%; Pred. No. 1.7e-282;
Matches 1350; Conservative 45; Mismatches 96; Indels 23; Gaps 8;

QY 1 MAAAAGNRASSGFFGARATSPGAGGGGALKASSAFAPAAAGLLREAGSGRERADRRR 60
Db 1 MAAAAGDRASSGFFGAAAASPGAGGGGALQGGAPAAAGALLRRTGSGRERADRRRQ 60
QY 61 QLRKVRVELDQLPEQLFLAASPASTSPSPADAGSGTGFQPVAVPPHGAASRG 120
Db 61 QLRKVRVELDQLPEQLFLTASPPCFTSPSPADAGAGSGFQPAAGPPPGAASRC 120
QY 121 GAHLTPESVAAPDSGASSPAAAPGKRAPAAPSPAPAAAGREMENKTLKGLHKMDRRP 180
Db 121 GSHSAELAAARDSGARSAGAEP-----PS-AAAPSGREMENKTLKGLHKMDRRP 170
QY 181 ERMIREKLKATCMPAWKHEWLERNRNRRGVPVVPVPIPKVGDGSENNHAAASPEVQASA 240
Db 171 ERMIREKLKATCMPAWKHEWLERNRNRRGVPVVPVPIPKVGDGSENNHAAALQGGQAGS 230
QY 241 ASPASKGRSPSGNSGRTVKSQGVRRKRVSPVPFQSGRITPPRRAPSPDGFSPYS 300
Db 231 AAPAFKGRSPSGNSGRTVKSQGVRRKRVSPVPFQSGRITPPRRAPSPDGFSPYS 290
QY 301 PEETRRVKNVNRARLYLLOQIGPNSFLIGDSDPNKYRVFVIGPQNCSCARGTCIHLFF 360
Db 291 PEETRRVKNVNRARLYLLOQIGPNSFLIGDSDPNKYRVFVIGPQNCSCRGTCIHLFF 350
QY 361 VMLRVFQLEPSPDMLWRKTLKNFVESLFQKYHRSRRSRKAPSNRTTQKFRVSMNSHT 420
Db 351 VMLRVFQLEPSPDMLWRKTLKNFVESLFQKYHRSRRSRKAPSNRTTQKFRVSMNSHT 410

QY	421	LSSSTSTSSSENSIKDEEQMCPICLLGMLEDSSLTVCEDGCRNKLHHHCHMSIWAEECR	480
Db	411	LSSSTSTSSSENSIKDEEQMCPICLLGMLEDSSLTVCEDGCRNKLHHHCHMSIWAEECR	470
QY	481	RNRREPLICCRSKWRSHDFYSHELSSPVDSPSIRAAQQOVTQOQPLACS--RNRQESNF	539
Db	471	RNRREPLICCRSKWRSHDFYSHELSSPVDSPSIRAAQQOVTQOQPLACS--RNRQESNF	530
QY	540	NLTHYGTQOIPRAYKDLAEPWTOFQGMELVCLFSRNWNVREMARLRSLSHDVSGALLLAN	599
Db	531	NLTHYGTQOIPRAYKDLAEPWTOFQGMELVCLFSRNWNVREMARLRSLSHDVSGALLLAN	590
QY	600	GESTGNSGGSGSSPGSGATSGSSOTSISGDVWFACCSVLSMWCADPVYKYVVAALKTLR	659
Db	591	GESTGNSGGSGSGSLSAGAASGSPSISGDVWFACCSVLSMWCADPVYKYVVAALKTLR	650
QY	660	AMLVYTPCHSLAERTIKLORLQPVVDITLVKCADANSTLSLSLLELCKQOAGELAV	719
Db	651	AMLVYTPCHSLAERTIKLORLQPVVDITLVKCADANSTLSLSLLELCKQOAGELAV	710
QY	720	GREILKAGSIGGGVDYVLYNCLNGOTSENNNQWELLGRCLIDIRLLEFPFPAEYPHIVST	779
Db	711	GREILKAGSIGGGVDYVLYNCLNGQABNNQWELLGRCLIDIRLLEISAEFYPHIVST	770
QY	780	DVSAQEPVEIRYKKLLSLTFALOSITDISHSMVGKLSRIYLSARMTVTPHVFESKLE	839
Db	771	DVSAQEPVEIRYKKLLSLTFALOSITDISHSMVGKLSRIYLSARMTVTPHVFESKLE	830
QY	840	MLSVSSSTHFTMRRRRLMAIADVEIAEAIOLGVEDTLDGQODSFLQASVPNNYLEFTEN	899
Db	831	MLSAGSSGHFARMRRRLMAIADVEIAEAIOLGSEDTLDGQODS--SOALAPPVY--PES	886
QY	900	SSPECTVHLEKTKGICATKLSASSEDISERLASTSVG--PSSSTTTTTTTEQPKPMVOT	958
Db	887	SSLEHTAHEKTKGUKATRLSASSEDISRLIAGVSGLPSSA-----TTEQPKPIVQT	940
QY	959	KGRPHSQCLNSPILSHSOLMPFALLSTPSSSTPSPAGTATDVSKHRLQGFIPCRIPSPAS	1018
Db	941	KGRPHSQCLNSPILS--PPOLMFPALISAPCSSAPSPAGSVTDAASKHRPAPVPCKIPSPAS	999
QY	1019	POTQRKFSLOFHRNCENKDSKLSPVFTQSRPLPSSNIHRPKPSRPTPGNTSKQGDPSK	1078
Db	1000	POTQRKFSLOFQTCSENRDSKLSPVFTQSRPLPSSNIHRKAKASRPVPGSTSKLGDASK	1059
QY	1079	NSMTLDLNSKCDQDFGCGSSNNAVIPSDSETVTPVEEKRCLDVNTFELNSSIEDLLEA	1138
Db	1060	NSMTLDLNSAQCDQDFGCGSSNGSAVIPSETAATPAEDKCRLDVNPENLSSIEDLLEA	1119
QY	1139	SMPSDDTVTFKSEVAVLSPKAEANDTYKDDVNHNQCKCKEKEABEPEALAIAMVASAS	1198
Db	1120	SMPSDDTVTFKSEVAVLSPKAEASDDTYKDDVNHNQCKCKEKEABEPEALAIAMVASAS	1179
QY	1199	QDALPIVPOLQVNGEDIILIQODTPETLPGHTKAKQYREDTEWLKQOIGLCAFSSCY	1258
Db	1180	QDALPIVPOLQVNGEDIILIQODTPETLPGHTKANEPIREDTEWLKQOIGLCAFSSCY	1239
QY	1259	QAQDVGTGLTMAYKQVTVYVRNTSSQEEVVEALREBEIRMHSHLNHPNIRMLGATCEKSN	1318
Db	1240	QAQDVGTGLTMAYKQVTVYVRNTSSQEEVVEALREBEIRMHSHLNHPNIRMLGATCEKSN	1299
QY	1319	YNLFIEWMAGSVAHLLSKYGAFKESVWNTYFOLLRLGLSYLHENQIITHRDVKGANLLID	1378
Db	1300	YNLFIEWMAGSVAHLLSKYGAFKESVWNTYFOLLRLGLSYLHENQIITHRDVKGANLLID	1359
QY	1379	STGQRLRIADFGAAARLASKGTGAGFQCOLLGTITAFMAPEVLRGOQYGRSCDVMYSGCA	1438
Db	1360	STGQRLRIADFGAAARLASKGTGAGFQCOLLGTITAFMAPEVLRGOQYGRSCDVMYSGCA	1419
QY	1439	IIEMACAKPPWNAEKHSNHLALIFKLTASATTAPSPSHLSPLGRDVALRCLLOPODRPP	1498
Db	1420	IIEMACAKPPWNAEKHSNHLALIFKLTASATTAPSPSHLSPLGRDVALRCLLOPODRPP	1479

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QY 1499 SRELLKHPVFTTW 1512
   |||||
Db 1480 SRELLKHPVFTTW 1493

RESULT 4
BCK1_YEAST STANDARD; PRY: 1478 AA.
ID BCK1_YEAST
AC Q01389; P32894;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Serine/threonine protein kinase BCK1/SLK1/SSP31 (EC 2.7.-.-).
GN BCK1 OR SLK1 OR SSP31 OR LAS3 OR YUL095W OR J0906.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
   [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=92186847; PubMed=1545797;
RX Costigan C., Gehring S., Snyder M.;
RA "A synthetic lethal screen identifies SLK1, a novel protein kinase
RT homolog implicated in yeast cell morphogenesis and cell growth.";
RL Mol. Cell. Biol. 12:1162-1178(1992).
   [2]
RP SEQUENCE FROM N.A.
RP MEDLINE=92104496; PubMed=1840547;
RX Irie K., Arai H., Oshima Y.;
RA "A new protein kinase, SSP31, modulating the SMP3 gene-product
RT involved in plasmid maintenance in Saccharomyces cerevisiae.";
RL Gene 108:139-144(1991).
   [3]
RP SEQUENCE FROM N.A.
RP MEDLINE=92107166; PubMed=1729597;
RX Lee K.S., Levin D.E.;
RA "Dominant mutations in a gene encoding a putative protein kinase
RT (BCK1) bypass the requirement for a Saccharomyces cerevisiae protein
RT kinase C homolog.";
RL Mol. Cell. Biol. 12:172-182(1992).
   [4]
RP SEQUENCE FROM N.A.
RP STRAIN=S288c;
RX MEDLINE=951176706; PubMed=7871887;
RA Miosga T., Boles E., Schaaff-gerstenschlaeger I., Schmitt S.,
RA Zimmermann F.K.;
RT "Sequence and function analysis of a 9.74 kb fragment of
RT Saccharomyces cerevisiae chromosome X including the BCK1 gene.";
RL yeast 10:1481-1488(1994).
   [5]
RP SEQUENCE OF 602-1104 FROM N.A.
RA Cusick M.E.;
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
CC 1- FUNCTION: SERINE/THREONINE PROTEIN KINASE INVOLVED IN A SIGNAL
CC TRANSDUCTION PATHWAY THAT PLAY A ROLE IN YEAST CELL MORPHOGENESIS
CC AND CELL GROWTH. THIS PATHWAY SEEMS TO STARTS BY SMP3; THEN
CC INVOLVE THE KINASE PKC1 THAT MAY ACT ON THIS KINASE. BCK1 PROBAB
CC PHOSPHORYLATES MKK1 AND MKK2 WHICH THEMSELVES PHOSPHORYLATE THE
CC MPK1 KINASE.
CC 1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC 1- SIMILARITY: BELONGS TO THE SRP/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE SUBFAMILY.
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or send an email to license@isb-sib.ch).
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DR EMBL; M84389; ; NOT ANNOTATED CDS.

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DR EMBL; D10389; BAA01226.1; -
DR EMBL; X60227; CAM42788.1; -
DR EMBL; X79233; CA834896.1; -
DR EMBL; Z49370; CA89389.1; -
DR EMBL; Z49369; CA89388.1; -
DR EMBL; M86604; AAA21179.1; -
DR PIR; S20117; S20117.
DR PIR; S22285; S22285.
DR PIR; J01118; J01118.
DR PIR; J01432; J01432.
DR HSP; P24941; ICKP.
DR SGD; S0003631; BCK1.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
KW ATP-binding; Phosphorylation.
FT DOMAIN 1175 1440
FT NP_BIND 1181 1189
FT BINDING 1204 1204
FT ACT_SITE 1303 1303
FT MOD_RES 1134 1134
FT VARIANT 1119 1119
FT VARIANT 1120 1120
FT VARIANT 1120 1120
FT VARIANT 1146 1146
FT VARIANT 1174 1174
FT CONFLICT 59 59
FT CONFLICT 79 79
FT CONFLICT 264 264
FT CONFLICT 279 279
FT CONFLICT 703 714
FT CONFLICT 795 795
FT CONFLICT 802 802
FT CONFLICT 808 808
FT CONFLICT 903 903
FT CONFLICT 919 919
FT CONFLICT 960 962
FT CONFLICT 1086 1104
SQ SEQUENCE 1478 AA; 164194 MW; D586C3A497A5BB33 CRC64;

Query Match 7.9%; Score 619; DB 1; Length 1478;
Best Local Similarity 21.0%; Pred. No. 5.2e-19;
Matches 332; Conservative 232; Mismatches 552; Indels 466; Gaps 64;

QY 224 EMNLAAEPGEVQAGAAPSKGR-----RSPSPG---NSPSGRTVKSESPGVRRKR 273
DB 24 KFGHQPTSSVASTKSSKSPRATRSKSIYDDIRSQFPNLTNPSTSSQFYES----- 74
QY 274 VSPVFFOSGRITPPRAPSPDGFSPSPETNRRVKNVYRARIYLILQOIPNSFLIGGDS 333
DB 75 -TPVIEQSFNWT-----TDDHISAGTLE-----NPTSFNTSSYK 107
QY 334 PDNKRYVFIGPONGSCAR---GTFCHLLFWMLRVFOLEPSDPLW---RKT----- 379
DB 108 NDN-----GPSSLSDSKSSGGNSVNSLFDKLLILSDPTDDEWTHRVTSNFKEHDF 161
QY 380 -----LKNFEVESLFQKYSRRSSRIKAPSRNTIOKFSVR-MSNS 418
DB 162 PESNLPFKKHQLFGRHFRIKLLAYDNPAVYKYLPTQTKTASYRFOQLLAKTKMTKNVTS 221
QY 419 H-----TLSSSTSTSSSNTSKDEEQMCPICLLGMLDEESLTVCEDGC-----RNK 466
DB 222 HIRKQSKALKSSSSSESISKSLKNSKQSE-DISNSRSTSEALSPTKSGPSKTDKKNF 280
QY 467 LHHCMSTIAECCRNRREPLICLRSKWRSHDFYSHELSPVDSPLSRAAQOQTVQOQ 526

DB 281 LH-----STSTHQTKSASSLYRRSFISLGRSSSSNASSAKSPSNKL-----SIPAR 328
QY 527 PLAGSRNQNESNENLTHYGTQIPPAYKOLAEPWIQVFGMELVGCFLFSRRNWNVREMLRR 586
DB 329 P-----HSIIIESNSTLKSASPPASPPS-----IFRRH-----HK 360
QY 587 LSHDVSALLANGESTGSGSGSGSGSPSGGATSGSS-----QTSISGVDVVEACCS 637
DB 361 SSSSESSLNSLFGSGIGEEAPTK-PNPOGHSLSSENLAKGSKKHETNVSSPLKOS--- 416
QY 638 VLSMVCADPVYKVVYAAKTLRAMLVVTPCHSLAERIKLQRLQLPQVVDTLVRCADANSR 697
DB 417 --SLPTSDDKGNLW---NKFKRSQIGVPSNVAVYTSQ-----ETPSLK---SNSS 461
QY 698 TSQLSISLTL-----LELCQOAGELAVGREILKAGSIGIGGVYVYVNLCLGN 744
DB 462 TATLTQTADVNIPIPSSSPPPIKTANRSLEIVSTEDTPKISSTTASFKETYPDCINPD 521
QY 745 QT---ESNNQELLGRCLIDRLLEFPAPFYPHIVSTDVSOAE-----PV 787
DB 522 KTVVPVNN-QKYSVKNFLLDQ-----KFYP-LKKTGLNDSNKVILYTKDNVSEVPL 572
QY 788 EIR-YKLLSLTLTALQSIDNSHSW-----GK 814
DB 573 NLKSVAKLSSEKESALATKLGINHKNVTFHMTDFDCDIGAAIPDDTLEFLKKSFLANTSGK 632
QY 815 LSRRYLSSARWTVVPHVFSKLEMLSVSSSTHTMRRLMAIADEVEIAEAIQ--LG 872
DB 633 IYIKDMKLOQRPAPLTSNNVPLKSVKSKSMRSGTSSLIASSTDVSVIVSSDITS 692
QY 873 VEDTLGQDSFLQASVFNNTLETENSSP-----ECTVHLEKTKGLOAT--KL 920
DB 693 FDEHASGSGRRYPQ--TPSYYYDVRVSNTPTEELNWNKIVLSHEENAPKMWKFTSPKL 750
QY 921 SASSDIERLASISVGPSSSTTTTTTTEQPKMWQTKGRPHSOCLNS-----PLSHH 975
DB 751 ELNLPDKGSKL-----NIPTITENESKSSQVLKDKDGTIDNHR 792
QY 976 SOLMF--PALSTPSSTSPVAGTADVSKHRLQGFIPRIPSPASQPTQRKFS-LQFHRNC 1033
DB 793 RESPYTKPELA-PKEAPKPPANTSPORTLSTSKCNKPIRLVRASTKISR----- 842
QY 1034 PENKDSKLSPVFTOSRPLPSNTHRP-KPSRPTPGNTSKQGDPSKSMTL-----D 1084
DB 843 -----KRSKLPPLQJLSSPIEASSSSDSSTSYTTPASTHVLIPIQYKGNAND 889
QY 1085 LNSSSKCD-DSFGCSS-----NSSNAVIPSDETVP---TP-----VVEKCR 1122
DB 890 VMRLKLTQDSTSTSPSLKMKQKVNRSNTSTVSTNSIFVSPSLKRGNSKRVVSSTSA 949
QY 1123 DVNTEINSSIEDLLEASMP-----SDTTVTFFKSEVAV-----LSPEKAEN 1163
DB 950 DIFEE-----NDITFADAPPMPDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSD 1004
QY 1164 DDTYKDDVNNHOKCKEKE-----AEEEAIAIAKASASODA 1201
DB 1005 STHSDEIFDSQTDOKMERKMTFRPSPEVYVQNLEKFFPRANLDKPILEGIASPTSPKS 1064
QY 1202 L-----PIVPOQVE-----NGEDIIIIQQDTP----- 1224
DB 1065 LDSLLSPKNVASSRTEPSTSPRPVPPDSYEFIDGLGKGNKPLNQAKTPKRTKRTIRTA 1124
QY 1225 -----ETLPGH-----TAKQPYREDTE--WLKGOQIGIG 1252
DB 1125 HEASLARKNSVKLKQNTKMWGTRAVETENHWSINAKNSKGEYKFAWMKGWIGK 1184
QY 1253 AFSSCYAQADVGTGLMAYQVTVYRNTSSQOEVE---VEALREIRMMHSHLNHNITRM 1309
DB 1185 SPGAVVLCNLNVTGEMMAYKQVE-VPKYSSQNEALISTVEALRSEVSTLKDHLNIVQY 1243
QY 1310 LGATCEKSNYLFIEWMAGGSVAHLLSKYGAFKESVWVNTYBOLLRGLSYLHENOIIRD 1369
DB 1244 LGPENKNYISLFLFYAGGSGVSLRMVGRFDEPLIKLTLTQVLKGLAYLHSGKILHRD 1303

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QY 1370 VKGANLLIDSTGQRLRIADFGAARLASKGTGAGFQGLLGTIAFMAPEVLRQQ-YGR 1428
      :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
Db 1304 KADNLLLDQDG-ICKISDFGSRK--SKDIYSNS-DMTMRGTVMFVWAPENVDTKQGVSA 1359
      :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
QY 1429 SCVWVSGCAIETIEMACAPPPNAEKSHLALIFKIASATAPAPISPHSLSGLRDVALR- 1487
      :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
Db 1360 KYDIWSLGCIVLEMFAGRPWS---NLEVVAAFPKIGKSKSAPPEDTTLPLISOIGRNF 1416
      :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
QY 1488 ---CLELOPQDRPPSRRELLKH 1506
      :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
Db 1417 LDACEINPEKRPANELLSH 1438
      :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |

RESULT 5
M3K3_MOUSE STANDARD; PRT; 626 AA.
ID AC Q61084;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Mitogen-activated protein kinase kinase 3 (EC 2.7.1.-)
DE (MAPK/ERK kinase kinase 3) (MEK kinase 3) (MEKK 3).
GN MAP3K3 OR MEKK3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96214986; PubMed=8621389;
RA Blank J.L., Gerlins P., Elliott E.M., Sather S., Johnson G.L.;
RT "Molecular cloning of mitogen-activated protein/ERK kinase kinases
RT (MEKK) 2 and 3. Regulation of sequential phosphorylation pathways
RT involving mitogen-activated protein kinase and c-Jun kinase."
RL J. Biol. Chem. 271:5361-5368(1996).
CC -!- FUNCTION: PREFERENTIALLY ACTIVATES P42/44 (ERK2/ERK1) MAP KINASES.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U43187; AAB03535.1; -
CC HSP; Q00534; IBI8.
CC MGD; MGI:1346674; Map3k3.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Euk_pkinase; 1.
CC SMART; SM00220; S_TKC; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC TRANSFERASE; Serine/threonine-protein kinase; ATP-binding.
CC DOMAIN 362 622 PROTEIN KINASE.
CC NP_BIND 368 375 ATP (BY SIMILARITY).
CC BINDING 391 391 ATP (BY SIMILARITY).
CC ACT_SITE 489 489 BY SIMILARITY.
CC SEQUENCE 626 AA; 70775 MW; 00BF2442C9E56E0B CRC64;

Query Match 7.1%; Score 559; DB 1; Length 626;
Best Local Similarity 29.9%; Pred. No. 6.4e-17;
Matches 167; Conservative 87; Mismatches 188; Indels 116; Gaps 21;

QY 1016 SASPQTKESFLOFHRNCPNKOSDKLSPVFTQSRPLPSN-----THRPKP----- 1062
      :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
```



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CC -----
DR EMBL; U78876; AB41729.1; -.
DR HSSP; Q00534; 1B18.
DR Genew; HGNC:6855; MAP3K3.
DR MIM; 602539; -.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 362 622 PROTEIN_KINASE.
FT NP_BIND 368 375 ATP (BY SIMILARITY).
FT BINDING 391 391 ATP (BY SIMILARITY).
FT ACT_SITE 489 489 BY SIMILARITY.
SQ SEQUENCE 626 AA; 70969 MW; E0F11F5082E9A810 CRC64;
Query Match 7.1%; Score 558.5; DB 1; Length 626;
Best Local Similarity 30.3%; Pred. No. 6.7e-17;
Matches 164; Conservative 85; Mismatches 191; Indels 101; Gaps 20;
QY 1016 SASPTQKRFSLQHRNCPENKDKSLSPVTQSRPLSSNIHRPKSRPPG----- 1068
DQ 129 SSSPHSEVSQRVIRASQASGADINTIYQPPERSRHLSSVSS-QNPGRSSPPGYVPERQQ 187
QY 1069 NTSKGDPSKSNMTLDLSSKCDSDFCGSSNNAVIPSDETFTVPEEKRDLVDNTEL 1128
DQ 188 HIRAGQ-----SYT-----SINSEGEFTPE-----TSQCMLDP----- 216
QY 1129 NSGIEDLLASPSDDTVV--TFKSEVAVLSPEKAENDTDYKD----- 1169
DQ 217 LSSAENSLSGSCQSLDRSADSPSFRKSRMSRAQSPFDRRQETSDRETQYDKGVKGTYTP 276
QY 1170 -----DYNHCKCKEKEAEEEAALAI-----AMAWSASODALPIVPO-----LQ 1209
DQ 277 RRYHVSVHHKDYSDGRFTFPRRHHQGNLFTLVPSRSLSTNGENKGLAVQYLDPRGLR 336
QY 1210 VNGEDIIIIQDTPETLPGHYKAQPTREDTEWLKGOIGLGAFFSSCYQADVTGTILM 1269
DQ 337 SADSSENALSQVRNVT-----KSP-SAPINWRGRGLLGQAGRYVLCYVDVDTGREL 388
QY 1270 AVKQTYVNTSSEGEVEVEALREETRMHSHLNHPNLINMLGATCEKSNYNL--PIEWNA 1327
DQ 389 ASKQVQFDPD-SPTSKEVSALCECEQLLKNQHERIVQYIGCLDRAREKITIPWEYMP 447
QY 1328 GGSVAHLLSKYGAFKESVINTVTEQLLRGLSYLHENQIHRDVKGANLLIDSTGQRLRIA 1387
DQ 448 GGSVKDQLKAYGALTESVTRKYTRQITLEGMSYLSHNMIVHRDIKANILRDSAG-NVKLG 506
QY 1388 DFGAARLAS---KGTGAGEFQGLGTIAFMAPEVLGRQQYQSCDVSVCATIEMAC 1444
DQ 507 DFGASRLQTIKMSGTG-----MRSVTGTYPWMSPEVIGSGRQADVWSLCTVYEMLT 562
QY 1445 AKPPWNAEKSHNLALIFKIASATAPSIHSLPSGLRDLVALRLELOQDPPRPSELK 1504
DQ 563 EKPPW-AEYEA--MAAIFKTIQATNPQLPSPHISEGRDF-LRRIFVEARQPSAEELIT 618
QY 1505 H 1505
DQ 619 H 619
RESULT 7
BYR2_SCHPO
ID BYR2_SCHPO STANDARD; PRT; 659 AA.
AC P28829;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein kinase byr2 (EC 2.7.1.-) (protein kinase ste8) (MAPK kinase
```

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kinase) (MAPKKK).
GN BYR2 OR STE8 OR SPBC1D7.05.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=91260705; PubMed=2046669;
RX Wang Y., Xu H.P., Riggs M., Rodgers L., Wigler M.;
RT "byr2, a Schizosaccharomycetes pombe gene encoding a protein kinase
capable of partial suppression of the ras1 mutant phenotype.";
RL Mol. Cell. Biol. 11:3554-3563(1991).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=93062799; PubMed=1435723;
RX Stykarsdottir U., Egel R., Nielsen O.;
RT "Functional conservation between Schizosaccharomycetes pombe ste8 and
Saccharomycetes cerevisiae Ste11 protein kinases in yeast signal
transduction.";
RL Mol. Gen. Genet. 235:122-130(1992).
[3]
RN SEQUENCE FROM N.A.
RP STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sources J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown S., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby I., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Jones K., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds S., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volktaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Aieger M., Schaefer M., Mueller-Auer S.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Roehet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Sipakowski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomycetes pombe.";
RL Nature 415:871-880(2002).
-1- FUNCTION: SERINE/THREONINE PROTEIN KINASE INVOLVED IN CONJUGATION
AND SPOULATION. IT IS THOUGHT THAT IT PHOSPHORYLATES THE BYR1
PROTEIN KINASE WHICH ITSELF PHOSPHORYLATES THE SPK1 KINASE..
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
-1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
-----
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EMBL; M74293; AAA35289.1; -.
DR EMBL; X68851; CAA48731.1; -.
DR EMBL; 298270; CAB10981.1; -.
DR PIR; A39723; A39723.
DR PIR; S30094; S30094.
HSSP; Q63450; 1A06.
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DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00536; SAM; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00454; SAM; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50105; SAM_DOMAIN; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Conjugation; Sporulation.
FT DOMAIN 4 67 SAM.
FT NP_BIND 394 658 PROTEIN_KINASE.
FT BINDING 400 408 ATP (BY SIMILARITY).
FT BINDING 423 423 ATP (BY SIMILARITY).
FT ACT_SITE 522 522 BY SIMILARITY.
FT ACT_SITE 522 522 BY SIMILARITY.
SQ SEQUENCE 659 AA; 73632 MW; 18CD78F1D1FABBCD CRC64;

Query Match 6.9%; Score 543.5; DB 1; Length 659;
Best Local Similarity 26.2%; Pred. No. 3e-16;
Matches 181; Conservative 115; Mismatches 259; Indels 137; Gaps 27;

QY 871 LGVEDTLGQDSFLQASVPNNVLETENSSP-----EC---TVHLEKGTG---KGLCAT 918
DB 46 LGIENTAKGQ--FLK---QRYLIR--EPRECIIRFIACNGQTRAVOSRGDYQKTLAIA 98
QY 919 KLSASSEDISERLASISVGPSSSTTTTTTTEQPKPMVQTKGRPHSQCLNSPLSHHSQL 978
DB 99 LKKFSLDASKFIVCV---SQSSRIKLITEEFKQI-----CFNSSSPERDRLI 144
QY 979 MFP-----ALSTPSSSTPVPAGTATDVSKHRLQGFIPCRIP 1015
DB 145 IVPKERPCPFEDLRWSIEIAQAALUSSQLSKPSSVLPTSTQKRSV-----RSN 198
QY 1016 SASPQTRKFSLQFHRNCENKSDKLSVVFQSRPLPSNLRPKPSRPTPGNTSKQGD 1075
DB 199 NAKP-----PESYQRPSELSINRISDFPD-----HQPILLEKLTISNLRNL 242
QY 1076 PSKNSMTLDNSSCKDDSFSGSSNSNAVIFSDFTVPVEKRLDVTNELNSI--ED 1134
DB 243 SINTSGHNL-----GNFGQILPRSSRRARPSELVCP-----SSLRISVAED 286
QY 1135 L--LEASMPSSDITVTFKSEVALSPEKAENDT-----YKDDVNHNOKCKEKEABE 1185
DB 287 VNELPRIDRGFDPLTVSTQIRSPPSLQKSTVMVGVEPLTQS--NGNEKSKKNVTFSE 344
QY 1186 -----BEALAIAMASAS--QDALPIVPOLOVENGEDIITIQDPTPETLPHTKAKQPYR 1238
DB 345 SAHGHNQVLSFSPGSPSPTEQSPISP--TSTTSDTNTLEEDTDD-----389
QY 1239 EDTEWLKGOQIGLGFASCYQAQDVGTLMAVKQVY--VRNTSEQEVVEALREIR 1296
DB 390 QSKWIRGALIGSGFGQVYLGNNASSGELMAVKQVILDSVESKDRHAKLIDLAGEIA 449
QY 1297 MMSHLNHPNIIRMLGATCSEKSNYLFIEWAGGSVAHLSKYGAFKESVVIYNTBOLLRG 1356
DB 450 LLOELSHETIVQVLSGNLNSDHLNIFLEYVPGSGVAGLLTMYGSEFTLVKFIQTLKG 509
QY 1357 LSYLHENQIIHRDVKANLLIDSTGRLRATDFGAARLA--SKGTGAGEFGQQLLGTIA 1414
DB 510 LEYLSRGVHRDIKAGILVNDKNG--KILISDFGISKLELNTSTSTKTGGARPSFGSGF 568
QY 1415 FMAPEYLRQOQYGRSDCVMSVGCATTEMACAKPPNNAEKSHNLALIFKIASATAPSTIP 1474
DB 569 WMAPEVVKQTMHTKEDYDIWSLGLVTEMLTSKHPY---PNCQMQAIFRIGE--NILPEFP 624
QY 1475 SHLSPGLRDVALRCLQLQDQDRPPSRELLKHP 1506
DB 625 SNISSAIDFLEKTAIDCNLRPTASELLSHP 656
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RESULT 8

M3K2_HUMAN STANDARD; PRT; 618 AA.

AC Q3Y2U5; 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Mitogen-activated protein kinase kinase 2 (EC 2.7.1.-)

DE (MAPK/ERK kinase kinase 2) (MEK kinase 2) (MEKK 2).

GN MAP3K2 OR MAPKKK2 OR MEKK2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

[1]

SEQUENCE FROM N.A.

SU B., Yang J.H., Xia Y., Karin M.;

"MEKK2 is involved in transducing T-cell co-stimulatory signals to the

JNK cascade.";

RT JNK cascade.";

RT activation.";

RL Mol. Cell. Biol. 20:2334-2342(2000).

CC -!- FUNCTION: PREFERENTIALLY ACTIVATES THE JNK/SAPK GROUP OF MAP

KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC MAP KINASE KINASE SUBFAMILY.

CC

CHARACTERIZATION.

CC MEDLINE=20180062; PubMed=10713157;

RA Cheng J., Yang J., Xia Y., Karin M., Su B.;

"Synergistic interaction of MEK kinase 2, c-Jun N-terminal kinase

(JNK) kinase 2, and JNK1 results in efficient and specific JNK1

activation.";

CC

CC -!- FUNCTION: PREFERENTIALLY ACTIVATES THE JNK/SAPK GROUP OF MAP

KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC MAP KINASE KINASE SUBFAMILY.

CC

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CC

EMBL; AF111105; AAD28547.1; -

DR Genew; HGNC:6854; MAP3K2.

DR InterPro; IPR000719; Euk_pkinase.

DR InterPro; IPR002290; Ser_thr_pkinase.

DR InterPro; IPR001245; Tyr_pkinase.

DR Pfam; PF00069; pkinase; 1.

DR PRINTS; PR00109; TYRKINASE.

DR ProDom; PD000001; Euk_pkinase; 1.

DR SMART; SM00220; S_TKc; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

KW Transferrase; Serine/threonine-protein kinase; ATP-binding.

FT DOMAIN 356 616 PROTEIN_KINASE.

FT NP_BIND 362 369 ATP (BY SIMILARITY).

FT BINDING 385 385 ATP (BY SIMILARITY).

FT ACT_SITE 483 483 BY SIMILARITY.

SQ SEQUENCE 618 AA; 69537 MW; 4C6B044BBF0A5401 CRC64;

Query Match 6.9%; Score 536.5; DB 1; Length 618;

Best Local Similarity 29.4%; Pred. No. 5.5e-16;

Matches 184; Conservative 78; Mismatches 188; Indels 175; Gaps 28;

QY 917 ATKLS--ASSEDI-----SERLASIS-VGPSSSTTTTTTTTTEQPKPMVQTKGRPHSQCL 967

DB 127 ATNLEPLPSLEDLNTVFGAEKRXLSIIGTTRSDRSPPPGYIDELHQVARNSSFSI 186

QY 968 NSS----PLSHHSQMLFFALSTP----SSSTPSV--PAGTATDVSKHRLQGFIPCRIPSA 1017

DB 187 NSEGEFIPESMEQMLDPLSLSPENSGSGCPSLSDPLGG-----ESYPSKRMPPRA 237

QY 1018 S--POTQKESLOFHCNCPENKDSKLSPVF-----TQSRPLSSNTHRPKPRPT-P 1067
Db 238 QSPDNHQEF-----SDYDNIFEFKFGKGGYPYRHYVSHHNDGKRKTFP 284
QY 1068 GNTSKGDPFSKNSMTLDLNSKCDPSFCSSNSSNAVPSDETFTPTVEEKRCLDVNTE 1127
Db 285 RARRTQG---NQLTSPV-SFSPTDLSLSTSGSS-----IFTPEYDSDRI---RR 327
QY 1128 LNSIEDLLEASMPSSDTITVTFKSEVAVLSPEKAENDTYKDDVNHNQCKEKEAEDEE 1187
Db 328 RGSDDID---NPLIT---VMDISP----- 344
QY 1188 ALAIAMASASQDALPIVQLQVENGEDIIIIQQDPTPETLPGHTRAKQPYREDTEWLKQ 1247
Db 345 -----PSRSP-----RAPTNWRGLCK 359
QY 1248 QIGLGFSSCYQADVGTGLMAVKQVTVYRNTSSQEEVFWALREERIMSHLHNPNI 1307
Db 360 LLGGAGFRVLYCYDYDTRELAVKQVQDPPD-SPETSKEVNALECEIQLLNFLHERIV 418
QY 1308 RMLGATC-----EKSNTNLTETWAGGSVAHLLSKYGAFKESVYVINTTEQLRLGSLYHEN 1363
Db 419 QYVG---CLRDPQEKTLISFMEYMPGGSIKDQLKAYGALTENGTRKYTROILSGVHYLSN 476
QY 1364 QIHRDVKANLLIDSTGRLRATDPAARLAS-----KGTGAGEFQGLLGTIAFWAPEV 1420
Db 477 MILHRDIKANILRDTG-NVRLGDFGASKRLQTCISGTG---MKSVTGTPTWMSPEV 531
QY 1421 LRQGGVGRSCDVWSGCAIETACAKPPNAEKNHLLIFKIASATTAPSPSHLSPG 1480
Db 532 ISQGVGRKADINSVACTVVMETEPWP-AEPEA---MAAIFKIATQTPNKLPPHVS DY 588
QY 1481 LRVDALRCLLELOQDPPRPSRELK 1505
Db 589 TRDF-LKRIFVEAKLRPSADELLRH 612

RESULT 9
ID STILL_YEAST STANDARD; PRT: 738 AA.
AC P23561;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase STE11 (EC 2.7.1.-).
GN STE11 OR YLR362W OR L8039.10.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE OF 22-738 FROM N.A.
RX MEDLINE=91115076; PubMed=2276621;
RA Rhodes N., Connell L., Errede B.;
RT "STE11 is a protein kinase required for cell-type-specific
transcription and signal transduction in yeast."
RL Genes Dev. 4:1862-1874(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=5288c / AB572;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Kucaba T., Fulton L., Gattung S., Greco T., Kirsten J.,
RA Johnston D., Johnston L., Langston Y., Latreille P., Le T.,
RA Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D.,
RA Rifkin L., Riles L., Taich A., Trevisan E., Vignati D.,
RA Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBSJ databases.
RN [3]
RP POSSIBLE FUNCTION.
RX MEDLINE=92331935; PubMed=1628833;
RA Cairns B.R., Ramer S.W., Kornberg K.D.;
RT "Order of action of components in the yeast pheromone response

pathway revealed with a dominant allele of the STE11 kinase and the
multiple phosphorylation of the STE7 kinase.";
RL Genes Dev. 6:1305-1318(1992).
CC FUNCTION: SERINE/THREONINE PROTEIN KINASE REQUIRED FOR CELL-TYPE-
SPECIFIC TRANSCRIPTION AND SIGNAL TRANSDUCTION IN YEAST. IT
IS THOUGHT THAT IT PHOSPHORYLATES THE STE7 PROTEIN KINASE WHICH
ITSELF, PHOSPHORYLATES THE FUS3 AND OR KSS1 KINASES.
CC -!- PATHWAY: RESPONSE TO PHEROMONE-INDUCED SIGNAL.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC
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CC
DR EMBL; X53431; CAA37522.1; -;
DR EMBL; U19103; AAB67571.1; -;
DR PIR; A36456; A36456
DR SGD; S0004354; STE11.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00536; SAM; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00454; SAM; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS0105; SAM_DOMAIN; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Pheromone response.
FT DOMAIN 41 105 SAM.
FT DOMAIN 436 733 PROTEIN KINASE.
FT NP_BIND 442 450 ATP (BY SIMILARITY).
FT BINDING 465 465 ATP (BY SIMILARITY).
FT ACT_SITE 600 600 BY SIMILARITY.
SQ SEQUENCE 738 AA; 83217 MW; A50D59800B346A41 CRC64;
Query Match 6.8%; Score 535; DB 1; Length 738;
Best Local Similarity 25.2%; Pred. No. 7.9e-16;
Matches 205; Conservative 117; Mismatches 215; Indels 276; Gaps 35;
QY 781 YQABPVEIRYKLLSLTFAL---QSIDNSHSMVGKL---SRRIVLSSA----- 824
Db 108 IEQVNLKLMKYSLSLSTATLSMNSLIPKHCVFILNDGSAKKVNVNCFNADSIKK 167
QY 825 RMVTVPHVFSKLEMLSVSSSTHPTRM-----RRRLMAIADEVEIAEAIQIGV 873
Db 168 RLRIPLPH-----ELLATNSNGEYTKMVQDYDFVLDYTRNVLHLLYDVELVTICH--A 219
QY 874 EDTLDGQDQDFLQASVPNNYLETENSPECTVHLEK---TGKGLCATKLSASSEDISER 930
Db 220 NDRVE-----KNRLIFVSKDQTPS-----DKAISTSKKLYLTLTALSQ----- 258
QY 931 LASISVGPSSSTTTTTEQPKMVQTKGRPHS-----OCLNSSPLS 973
Db 259 -----VGPSSSNL-----LAQNKGISHNNAEKGKLRIDNTEKDRIQIFNQR-- 300
QY 974 HHSQLMFFALSTPSSSTPSVPAGTATDYSKHLQGFICRIPSPSPQPKFSLQFHRNC 1033
Db 301 -----PSEFISTNLAGFPHTDMRLQ-----KTMRE----- 327
QY 1034 PENKDSKLSPVFTQSREL--PSSNIHRPKPSRTPGNTSKQGPFSKNSMTLDLNSSKC 1091
Db 328 -SFRHSARLS--IAQRRPLSAESNNI-----GD----- 352

```
QY 1092 DDFGSSSSNAVIPSDETFVPEVKCRDLVDNTELNSSIEDLEASMPSSDITVTFKS 1151
Db 353 -----ILLKHSNAV---DMALGLDQ-----TLSSKL-----DTI----- 381
QY 1152 EVAVLSPERANDTDYKDDVNNHQQCKEKMEAEESALAIAMAMSASQDALPIVPOLOVE 1211
Db 382 KIPKLAHRPEDNDAS-----NQELLSVESGEES-----DHDF----- 417
QY 1212 NGEDIIIIQDDTETPLGHTKAKQPYREDTEWLKGOQIGLGFSSCYOQADVCTGTLMAV 1271
Db 418 -GSDIV-----SLP--TKIATP-----KNLKGACIGSGSGVYLCMNAHTGELMAV 464
QY 1272 KQTYVYRNT-----SSEQEE-----VVEALRE 1293
Db 465 KOVEIKNNNVGPTDNNKQANSDENNEQEQBKIEDVGAVSHPKNTQNIHRKMDVALQH 524
QY 1294 EIRMSHLNHPNIIIRMLGATCESNYNLFIEWMAGSVAHLLSKYCAFESVIVNTTEOL 1353
Db 525 EMLLKELHENIVTYGASQEGGNLIFLEYVPGSVSMLNNGYFFESLITNTROI 584
QY 1354 LRGLSVLHENQIIRHVDKGANLLIDSTGQRLRIADFGAARLASKGTGAGEQGLLGTI 1413
Db 585 LIGVAVLHKNNIIRHDIKGANILIDIK-CVKITDFGISKLSPLNKQK-RASLQGSV 642
QY 1414 AFMAPEVLRCQQYGRSCDVWSVCCALIEMACAKPPNAEKSHNLALIKIASATAPSI 1473
Db 643 FWSPEVYKOTATKADINWSTGCVIEMFTGKHP---PDFSQMAIFKIGTNTT-PEI 698
QY 1474 PSHLSPGLRDVALRCLLELOPDRPPSRELLKHP 1506
Db 699 PSNATSEKFNFLKAEFLDYQYRPSALELLOHP 731

RESULT 10
M3K2_MOUSE
ID M3K2_MOUSE STANDARD; PRT; 619 AA.
AC Q61083;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Mitogen-activated protein kinase kinase 2 (EC 2.7.1.1)
DE (MAPK/ERK kinase 2) (MEK kinase 2) (MEKK 2).
GN MAP3K2 OR MEKK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96214986; PubMed=8621389;
RA Blank J.L., Gerwins P., Elliott E.M., Sather S., Johnson G.L.;
RT "Molecular cloning of mitogen-activated protein/ERK kinase kinases
RT (MEKK) 2 and 3. Regulation of sequential phosphorylation pathways
RT involving mitogen-activated protein kinase and c-Jun kinase."
RL J. Biol. Chem. 271:5361-5368(1996).
CC -1- FUNCTION: PREFERENTIALLY ACTIVATES THE JNK/SAPK GROUP OF MAP
CC KINASES. PHOSPHORYLATES MEK1 OR JNK MAP KINASE IN VITRO.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE KINASE SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U43186; AAB03536.1;
CC MGD; MGI:1346873; Map3k2.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
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DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TAC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 356 616 PROTEIN KINASE
FT NP_BIND 362 369 ATP (BY SIMILARITY).
FT BINDING 385 385 ATP (BY SIMILARITY).
FT ACT_SITE 483 483 BY SIMILARITY.
SQ SEQUENCE 619 AA; 69835 MW; 799A35218DDE7C41 CRC64;

Query Match 6.8%; Score 531; DB 1; Length 619;
Best Local Similarity 28.4%; Pred. No. 9.4e-16;
Matches 168; Conservative 78; Mismatches 214; Indels 132; Gaps 24;

QY 944 TTTTTEQPKMVQTKGRPHSQCLNSPLSHSHQLMFALSTPSSSTPSVAGATADYSK 1003
Db 124 STQATNLEFSPSED-----LNTPLGAERKRLSVGPPNDRSSPPGYIPDILH 175
QY 1004 H--RLQGIPCR-----IPASAPQQRKFSLQFHNCENKDSKLSVFTQSRPLPSN 1056
Db 176 QIARNGSTSIINSEGEFIPESMDMLDPLSL-----SPENSGSGSCPSL---DSPLDGES 228
QY 1057 IHRPKPSRTPGNTSKQDPSKNSMTDLNSSSKCDDDSFGCSS-----NS 1101
Db 229 Y--PKSRMP-----RAQSVPDNHQEFIDYD--NPIFEKFGKGTYPRRYHYSHHQEYND 279
QY 1102 SNAVIPSDETFVPEVKCRDLVDNTELNSSIEDLEASMPSSDITVTFKSEVAVLSPEKA 1161
Db 280 GRKTFP-----RARTQGTSTFRSPV-----SFTDHSLSYSSGSSVETPE-- 320
QY 1162 ENDITYKDDVNNHQQCKEKMEAEESALAIAMAMSASQDALPIVPOLOVENGEDIIIIQQ 1221
Db 321 -----YDSDSRIRRR-----GSDI----- 333
QY 1222 DTPE-TLGHAKAKOPYREDTEWLKGOQIGLGFSSCYOQADVGTGLTLMAYKQTYVNT 1280
Db 334 DNPTITVTDISPPSRAPRNTNRLGKLGOGAGRGVYLCVDVDTGRELAVKQVQF-NPE 392
QY 1281 SSEQEEVVEALREIRMSHLNHPNIIIRMLGATC-----EKSNNLFIEWMAGSVAHLLS 1336
Db 393 SPETSKEVNALECEIQLLNLLHRIYQYVG--CLRDQEKTLSTFMEELSPGSIKQDLK 450
QY 1337 KYGAPKESVINYTQLLRGLSYLHENQIIRHVDKGANLLIDSTQRLRIADFGAARLA 1396
Db 451 AYGALTENVTRYKTRQILEGVHYLSNMIVHRDIKGANILRDSTG-NIKLGDGFGASKRLQ 509
QY 1397 S---KGTGAGEFGQGLLGTIAFMAPEVLRCQQYGRSCDVWSVCCALIEMACAKPPNAEK 1453
Db 510 TICLSGTG---MKSVTGTPYMWSPVISGEYGRKADINWSVACTVVMLETKPFW-AEF 564
QY 1454 HSNHLALFKIASATAPSIHSLSPGLRDVALRCLLELOPDRPPSRELLKH 1505
Db 565 EA--MAAIFKIAITQPTNPKLPHPVSDYTRDF-LKRIFVEAKLRPSAEELLRH 613

RESULT 11
MKHL_SCHPO
ID MKHL_SCHPO STANDARD; PRT; 1116 AA.
AC Q10407;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE MAP kinase kinase kinase mkhl (EC 2.7.1.-).
GN MKHL OR SPACIF3.02C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN [1]
```


RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND MUTAGENESIS OF LYS-1371.
RC TISSUE=Fetal liver, and Skeletal muscle;
RX MEDLINE=97449143; PubMed=9305639;
RA Takekawa M., Posas F., Saito H.;
RT "A human homolog of the yeast Ssk2/Ssk22 MAP kinase kinase,
RT MTK1, mediates stress-induced activation of the p38 and JNK
RT pathways";
RL EMBL J. 16:4973-4982(1997).
RN [2]
RP SEQUENCE OF 68-1607 FROM N.A. (ISOFORM B).
RC TISSUE=Bone marrow;
RX MEDLINE=97191544; PubMed=9039502;
RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayashi Y.,
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. VI.
RT The coding sequences of 80 new genes (K1AA0201-K1AA0280) deduced by
RT analysis of cDNA clones from cell line KG-1 and brain";
RL DNA Res. 3:321-329(1996).
CC -1- FUNCTION: ACTIVATES THE CSBP2, P38 AND JNK MAPK PATHWAYS, BUT NOT
CC THE ERK PATHWAY. SPECIFICALLY PHOSPHORYLATES AND ACTIVATES MAP2K4
CC AND MAP2K6.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN HEART, PLACENTA,
CC SKELETAL MUSCLE AND PANCREAS, AND AT LOWER LEVELS IN OTHER
CC TISSUES.
CC -1- DOMAIN: THE N-TERMINAL NON-CATALYTIC DOMAIN (1-606) CONTAINS AN
CC ESSENTIAL DOMAIN FOR THE DOMINANT-INHIBITORY EFFECT.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE SUBFAMILY.
CC
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CC
CC EMBL; AF002715; AA868804.1; .
CC EMBL; D86968; BAAL3204.1; .
CC HSP; P24941; 1HCL.
CC Genew; HGNC:6856; MAP3K4.
CC MIM: 602425; .
CC InterPro; IPR00719; Euk_pkinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Euk_pkinase; 1.
CC SMART; SM00220; S_TKc; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Alternative splicing. 7
FT DOMAIN 4 POLY-ALA.
FT DOMAIN 25 38 POLY-PRO.
FT DOMAIN 1190 1201 POLY-ALA.
FT DOMAIN 1342 1600 PROTEIN_KINASE.
FT NP_BIND 1348 1355 ATP (BY SIMILARITY).
FT BINDING 1371 1371 ATP (BY SIMILARITY).
FT BINDING 1462 1462 BY SIMILARITY.
FT ACT_SITE 1475 1223 MISSING (IN ISOFORM B).
FT VARSPIC 1371 1371 K->R: LOSS OF ACTIVITY.
FT MUTAGEN 1371 791 I -> R (IN REF. 2).
FT CONFLICT 791 791
SQ SEQUENCE 1607 AA; 181550 MW; 24BC4597730B5287 CRC64;
Query Match 6.4%; Score 502.5; DB 1; Length 1607;
Best Local Similarity 19.7%; Pred. No. 4.5e-14;
Matches 288; Conservative 239; Mismatches 574; Indels 363; Gaps 59;
QY 169 TLKGLHKDDDRPERMIREKLKATCMAPKAWHEWL---ERRNR-----208
DB 370 SLQALQKDYKYAANDFDQVQALCL-----WLNITKDLNOKLRMGTVLGIKNLSDIG 423

QY 209 GPVVVKPIPVKGDGSENMHAAESPGEVQAASASPASKGRSPSPGNSGRTVKSESPG 268
DB 424 WPVFEIPSPRSGKNEPEYEGDDTEGELKELESS-----TDESEEEQ 465
QY 269 VRRKRVSPVFPQSGRITPPRAPSPDGFSPISPEETNRVNVKVMARLYLLQOIGPNSFL 328
DB 466 ISDPV-----PEIRQPIDNSFDIQSRDCISK-----LERLESEDDS 503
QY 329 IGGDSPDNKYRVFIGPQNCSCARGTFCIHLLFVMLRVQLPEPSDPMLMRKTLKNEVESL 388
DB 504 LQWGPD-----WSTEAG-FSRCLTSTVRFV-----DKALKQMLRKL 542
QY 389 FOKYHS-----RRSRIKAPSNTTKQFVSRMSNHTLSSSSTSTSSSE--NSIKDE 438
DB 543 ILRLHKLMDGSLQARIALVKNDREVESEFPDPMWGDYVQLSRTSPSESEKSAVSE 602
QY 439 EQQMCPICLLGLMD---EESLTVCEDGCRNKLH--HHCMSIWADEECRRNEPLICPL-- 490
DB 603 E-----LKANDLPSEPAFLV---CRVLLNVHCEKLRLEQ-RPAGEPSLLSIKQ 650
QY 491 ----CRSKWRS-----HDFYSHELSPVSPSSLRARAAQQTVOOQPLAGSRNRQESNF 539
DB 651 LVRECKEVLKGLLMKQYQFQMLQEVLEDEKP-----DCNI 687
QY 540 NLTHYGTQIIPAYKDLAEPWQVF-----GMELVGCCLFSRNN-----VR--EMAL 584
DB 688 DAFEDLHKMLMVFYDMKSWIOMLQOLPQASHSLKNLEEWNTKETHYIRGEQAQ 747
QY 585 RRLSHDVSGALLIANGESTGNSGGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 644
DB 748 GKLFCDIAGMLLKSTGTFLEFGLOESCAEFWTSADSSASDEIIRSVIE-----ISRALK 802
QY 645 DPVYKYVVAALTRAMLYVTCHSLAEIKLQRLLOPVVDI-----LVKCADANSRTSQ 700
DB 803 ELFHAEAREASKALGPAKMLRDLKLEIAAEFRLSAPVRDLDLVKSKYQVQIPLGLENLQ 862
QY 701 LSISTLLELCKGAGELAVGREILKAGSIGIGVD-----YVINCILGNQTES 748
DB 863 MFVPDYL-----AEKSIILQLNAAA-----GKDCSKSDVDVLIDAYLLTKHGDRARD 912
QY 749 N-----NQOELLGRCLDLRLLEFPFAEPYPHIVSTDVQAQPEVRYKLLSLTLTALQ 803
DB 913 SEDSWGTWEAQ-----PVKVVQVETVDTLRSMQVD-----NLLLVNQ 951
QY 804 SIDNSHSMVGKLSRRIVLSSARVTVT-----PHVFSKLEMLSVSSSTHTFRMRRL 856
DB 952 S---AHLTI---QRKAFQOSIEGLMTLCQEQTSQSPVIAKALQQLA-----991
QY 857 MAIADEVEIAEATQLGVEDTLDGQDSFLQASVPNNYLETENSSPECTVHLEKGTG----912
DB 992 ---NDALELCNRISNAT-DRVDHMF*SEFDAEYDESESVTLQOYYREAMIQGYNFGFEYH 1047
QY 913 KGLCATKLSASSEDISERLASISVGPSSSTTTTITTTTQPKPMVQTKGRPHSQCINSSPL 972
DB 1048 KEVRLMSGFROKIGDKYISFARKWNYVLTKEGSRGTRPWNATQGFLOAIEPAFI 1107
QY 973 SHHSQMLFPALSTPSSSTPVPAGTATDVSKHRLQGFIPCRIPASAPQTKRKSLOFHRN 1032
DB 1108 SALPEDDDELSLQALMNECIGHVIG-----KPH-----SPVT--GLYLAIHRN 1147
QY 1033 CPENKSDSKLSPVTTQSRPL-----PSSNIHREKP-----SRPTGNTSKQGPDSKN 1079
DB 1148 SP-----RPMKVPFCHSDPPNPHLIPTPEGFTSRMPSDARGHSGPAAA 1192
QY 1080 SMTLDLSSSKCDDSFCCSSNSSNAVIPSDETFTVPEKCRDLVDNTELNSSIEDLEAS 1139
DB 1193 AAAAAAASRRSPSGG-----DSVLPKS-----ISSADTRGSS 1227
QY 1140 MPSSDITVTFKSEVAV-----LSPEKAENDDTYK--DDVNHQCKE--KMEAEEREAL 1189
DB 1228 VPENDRLASIAAEQLFSLRSHSSPTEERDEPAYPRGDSGSGSTRSRWELTSLISQSKDTA 1287

QY 1190 ATAMASQDALPIVQLOVNGEDIIIOQ--DTPETLPG--HTKAKQPYREDTEWLK 1245
Db 1288 SKLGPIEALQKSRVFEKRYREMRKNIIGQVCDTPKSYDNVHVGLR---KVTFKWR 1344
QY 1246 GOQIGLAFSSCYQADQVGTGLMAVKQTYVVRNTSSQBEVVEALREIRMMSHLNHPN 1305
Db 1345 GNKIGEGYQKYVTCISVDTELMAKKEIRQFN-----DHKTITKETADELKIFEGIKEPN 1400
QY 1306 IIRMLGATCEKSNYNLFIEMWAGGVAHLLKYGAFKESVINTYEQLLRGLSVLHENOI 1365
Db 1401 LVRVFGVELHREMYIFEMYCEGILEE-VSRLG-LQEHVIRLYSKQITAINVLHREHI 1458
QY 1366 IHRVKGANLLIDSGORLRIADGAARLASKG-TGAGEFGQGLLGTIAFMAPEVL--- 1421
Db 1459 VHRDINGANIFTSSG-LIKLGDGFCVKLKNNAQTMPEV-NSLTGAAVNAPEVITRA 1516
QY 1422 RQOYGRSDVMSVCAITEMACAPPMNAEKSHNLALIFKIASATAPSPSHLSPL 1481
Db 1517 KEGHGRADINSLGCVIEMVTKRPWEYEH-NFQIMYKVGNG-HKPPPIERLSPEG 1573
QY 1482 RDVALCELEQODRPPSRRLKKH 1505
Db 1574 KDFLSHCLESDFKRWMTASQLLDH 1597

RESULT 13
M3K4_MOUSE
ID M3K4_MOUSE STANDARD; PRT; 1597 AA.
AC 008648; 008649; 070124;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mitogen-activated protein kinase kinase kinase 4 (EC 2.7.1.1.)
DE (MAPK/ERK kinase kinase 4) (MEK kinase 4) (MEKK 4).
GN MAP3K4 OR MEKK4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RC TISSUE=Brain;
RX MEDLINE=97236778; PubMed=9079650;
RA Gerwins P., Blank J.L., Johnson G.L.;
RT "Cloning of a novel mitogen-activated protein kinase kinase kinase, MEKK4, that selectively regulates the C-Jun amino terminal kinase pathway".
RT J. Biol. Chem. 272:8288-8295(1997).
RL [2]
RN SEQUENCE OF 363-1049 FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Ectoplacental cone;
RX MEDLINE=97422605; PubMed=92268631;
RA Schweifer N., Valk P.J., Delwel R., Cox R., Francis F.,
RA Meier-Ewert S., Lehrach H., Barlow D.P.;
RT "Characterization of the C3 YAC contig from proximal mouse chromosome 17 and analysis of allelic expression of genes flanking the imprinted Igf2r gene".
RT Genomics 43:285-297(1997).
RL GENOMICS 43:285-297(1997).
CC -!- FUNCTION: ACTIVATES THE CSBP2, P38 AND JNK MAPK PATHWAYS, BUT NOT THE ERK PATHWAY. SPECIFICALLY PHOSPHORYLATES AND ACTIVATES MAP2K4 AND MAP2K6.
CC -!- SUBCELLULAR LOCATION: LOCALIZED IN PERINUCLEAR VESICULAR-LIKE STRUCTURES, PROBABLY GOLGI-ASSOCIATED VESICLES.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGH EXPRESSION WAS FOUND IN SKELETAL MUSCLE, KIDNEY, TESTIS FOLLOWED BY HEART BRAIN AND LUNG.
CC LOW EXPRESSION WAS FOUND IN SPLEEN.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MAP KINASE KINASE KINASE SUBFAMILY.
CC
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CC
CC -----
CC EMBL; U85607; AAC53126.1; -
CC EMBL; U85608; AAC53127.1; -
CC EMBL; U66240; AAC08286.1; -
CC HSP; P24941; IHL.
CC DR MGI:1346875; Map3k4.
CC DR InterPro; IPR000719; Euk_pkinase.
CC DR InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC PRODOM; PD000001; Euk_pkinase; 1.
CC SMART; SM00220; S_TKc; 1.
CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Alternative splicing.
FT DOMAIN 1178 1182 POLY-ALA.
FT DOMAIN 1332 1590 PROTEIN KINASE.
FT BIND 1338 1345 ATP (BY SIMILARITY).
FT BINDING 1361 1361 ATP (BY SIMILARITY).
FT ACT_SITE 1452 1452 BY SIMILARITY.
FT VARSPLIC 1162 1213 MISSING (IN ISOFORM B).
FT CONFLICT 363 364 SL -> NS (IN REF. 2).
FT CONFLICT 473 473 T -> A (IN REF. 2).
SQ SEQUENCE 1597 AA; 179948 MW; E84AEAAE92D103A4 CRC64;
Query Match 6.1%; Score 475; DB 1; Length 1597;
Best Local Similarity 20.4%; Pred. No. 6.4e-13;
Matches 301; Conservative 211; Mismatches 576; Indels 386; Gaps 66;
QY 169 TLKGLHKWDDPEERWIREKLKATCMPAKWHEWL---ERRNRGPPVVKVPVKGDSGEM 225
Db 363 SLQALQKDYERVAADKDFRVQALCL-----WLNITDLQKLRIMGTVLGIK-NLSDI 415
QY 226 NHLAAEPCEVQASAAASPARRSPSPGNSPGSGRTVASE-----SPGVRRKRVSPVPF 279
Db 416 GMPVEIP-----SP-----RPSKGYEPEDEVEDELRELESGTEESDEPTP- 460
QY 280 QSGRTTPPRAPSPDGFSPYPE-----ET---NRNVKVMRRLVLLQQTGPNSEFLGG 331
Db 461 -----SPRVDELRLSTDTILDSRSQGVSRK-----LERLESEDSIGW 499
QY 332 DSPDNKRYVFIGPQNCSCARGTFCIHLLFVMLRVFQLEPDPMLWRKTLKNFEVESLFQK 391
Db 500 GTAD-----CGPE---ASR-----HCLTSIYRPFV-----DKALKQMLKRLIIR 536
QY 392 YHS-----RSSRIKAPSRNTIQKFVSRMSNSHTLSSSTSTSSSENSIKDEEQMC 443
Db 537 LHKLMNGSLQARVALVKDDRVERFSDFGPMWGDYVOLSGTPPSS-----EQKC 587
QY 444 PICLLGMLDEESITVCEGD-----CRNKLH---HHCMSIAECCRRNREPLICPL-----C 491
Db 588 SAVSWEEELAMDLPSEPAFLVLCRVLLNVIHECLKLRLQEQ-RPAGEPSLLSIKOLVREC 646
QY 492 RSKWRSHDFYSHLSFVDPSPSLRAAQQTQQQPLAGSRNRQNSFNLTHTVGTQQIPP 551
Db 647 KEVLY-----GGLLMKQYQFMLOEVGLGLEXTCNDMDAFEDLQKMLM 690
QY 552 AYKDLAEPWTQVF-----GMELVGCILFSRNW-----VR---EMALRRLSHDVSGALL 596
Db 691 VYFYDVRNLTQMLQQLQPOASHLSKLNLEEWNFTEKTHIYIRGGEAQAGKLCFCDIAGMLL 750
QY 597 LANGE-----STGNSGGSS-----GSSPSGGA 618
Db 751 KSTGSPFLESLQESCAELWTSADNGADELRLRSVIEISRALKELFHEAREHRSKALGFA 810
QY 619 TSGSSOTISGDVVEACCS---VLSWVCADPVYKVVYVAALKTLRAMLVYTPCHSLAERIKL 676

Db 811 KMLRKDLTAIEFVLSASARELLDALKAKQYVKVQIPGLENLH---VFVP-DSLAEEKKI 866
QY 677 QRLQPVVDITILVKA---DANSRTSLSISITLLBLCKGQAGELAVGREILKAGSIGGG 733
Db 867 --ILQ-----LLNAATGKDCSKDDVDFMDFALLTK--HGDR----- 901
QY 734 VDYVNLCLNGTESNNWQELGLRCLLDRLLEFPABFYHIVSTVDSQAEPVE-IRYK 792
Db 902 -----RDESGWGWTARAVKI-----VPQVETVDLRSK 931
QY 793 KLLSLTLFALQSIDNSHSMGVKLSRIYLSARMVTVPH-----VFSKLEMLSVSS 845
Db 932 QVDNLLLVVNES---AHLV---LORKAFOQSIEGLMVRHEQTSSQPIAKGLQOLK--- 982
QY 846 SHFTFEMRRRLMAIADEVEIAEAIQGLVEDTLDGQODSF---LQASVPNNYLETTENSSP 902
Db 983 -----NDALCELNRI-----SDAIDRVDMFTLEFDEAVESESATLQOYR 1024
QY 903 ECTVHLEKTG---KGLCATKLSASEDISERLASISVGPSSSTTTTITTTTTPQPMVOT 958
Db 1025 EAMIOGYNFGEVHKVWRLMSGEFRQKIDKYISFAQKMMVNLTKCESGRGTRPRWAT 1084
QY 959 KGRPHSOCLNSPLSHSOLMPALSTPSSSTPSPVAGTATDVSKHRLQGFIPCRIPAS 1018
Db 1085 QGFDFLQAIAPAFISALPEDDFLSIQALMNECIGHVIG-----KPH-----S 1126
QY 1019 PQQRKESLQFHRCNCPENKDSKLSVFTQSRPLSPSNIRHKPSR---PTPGNTSKOG 1074
Db 1127 PVT-----AIHNSP-----RPVKVPRCHSDPPNPHLIITPEGFSTRS 1165
QY 1075 DPBK-----NSWTLDNSKDDKDDSGCSSNSNAVIPDEIVFTVBEKCRLDVNTLNL 1129
Db 1166 VPSDARTHNSVAAAAAARAATAAGRPFGPGGGDVPAK-----PVNT----- 1209
QY 1130 SSTEDLEASMPSSDITVTFKSEVAV-----LSPEKAENDDTY---KDDVNNKQCKE-- 1179
Db 1210 --APDRGSSVPENDRLASTAAELQFRSLRSHSSPTEERDEPAYPRSDSGSTRRWELR 1267
QY 1180 KMEABEEALAIAMASQADALPIVQLOVENGEDIIIIQ--DPEPLPG--HTKAKQ 1235
Db 1268 TLISQTSKASKOGPIAIGKSVLFEERYREMRKNIIGVCDIPKSDVNVNHHVGLR- 1326
QY 1236 PYREDTEWLGQGTGLGAFSCYQADQVGTGLMAYKQVTVRNTSSEQEVEVVEALREEI 1295
Db 1327 --KVTFKQWQNGIGEGYQKVTCTISVDTGELAMKEIRFQPN---DHKTIKETADEL 1380
QY 1296 RMGSHLNPHNIIRMLGATCKSNYNLEFEMWAGSVNAHLLSKYGAPKESVINYVTEQLLR 1355
Db 1381 KIFEGIKHPLNLYFYGVELHREEMYIFMEYCDDEGTLEE-VSRIG-LQEHVIRLYTKQIV 1438
QY 1356 GLSYLHENOITHRDVKGANLLIDSTGQRLRIADFGAARLASKG-TGAGVFGQQLLGTIA 1414
Db 1439 AINVLEHGVHRIKGANIFLTSSG-LIKLGDGCSVKLKNNAQTMPGEV-NSTLGTAA 1496
QY 1415 FMAPEVL---RGOQYGRSDVWSVGCATIEMACAKPPWNAEKSHUALIFPKIASATTAP 1471
Db 1497 YMAPEVITRAKGEHGRAADTSLGCVVIEVMVTGKRPHEHYEH--NFOIMYKVGMG-HKP 1553
QY 1472 SIPSHLSPGLRDVALRCLELQPODRPPRSRELLKH 1505
Db 1554 PIPERLSPGKAFSLHCLSDPKIRWTASQLLDH 1587

RESULT 14

ID WISA_SCHPO STANDARD; PRT; 1401 AA.
AC 014299; 987062; 092384;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE MAP kinase kinase kinase wisa4 (EC 2.7.1.-) (MAP kinase kinase kinase
DE waki1) (MAP kinase kinase kinase waki1).
GN WISA4 OR WAK1 OR WIK1 OR SPAC931.02.

OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98026892; PubMed=9321395;
RA Samejima I., Mackie S., Pantes P.A.;
RT "Multiple modes of activation of the stress-responsive MAP kinase
RL pathway in fission yeast";
RN EMBL J. 16:6162-6170(1997).
RP [2]
RX SEQUENCE FROM N.A.
RA STRAIN=972;
MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feitwell T., Fraser A.,
RA Gentles S., Gobie A., Hamlin N., Harris D., Hidaigo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford J., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkhardt G., Aert R., Robben J., Grymonprez B.,
RA Weijens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Rhode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerruti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe";
RL Nature 415:871-880(2002).
RN [3]
RP SEQUENCE OF 96-1401 FROM N.A.
RX STRAIN=972;
MEDLINE=97282620; PubMed=9136929;
RA Shieh J.C., Walkinson M., Buck V., Morgan B., Makino K.,
RA Millar J.B.A.;
RT "The Mts4 response regulator coordinately controls the stress-
RL activated Waki1-Wis1-Styl MAP kinase pathway and fission yeast cell
RN cycle";
RN Genes Dev. 11:1008-1022(1997).
RP [4]
RX SEQUENCE OF 457-543 FROM N.A.
RA STRAIN=972;
MEDLINE=97331762; PubMed=9188094;
RA Shiozaki K., Shiozaki M., Russell P.;
RT "Mts4 mitotic catastrophe suppressor regulates the fission yeast cell
RN cycle through the Wki1-Wis1-Spc1 kinase cascade";
RN Mol. Biol. Cell 8:409-419(1997).
CC -1- FUNCTION: INVOLVED IN A SIGNAL TRANSDUCTION PATHWAY THAT IS
CC ACTIVATED IN UNDER CONDITIONS OF HEAT SHOCK, OXIDATIVE STRESS OR
CC LIMITED NUTRITION. UNLIKE WIK1, IT IS NOT ACTIVATED BY CHANGES IN
CC THE OSMOLARITY OF THE EXTRACELLULAR ENVIRONMENT. ACTIVATES THE
CC WIS1 MAP KINASE BY PHOSPHORYLATION.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).

DR EMBL: 298763; CAB11500.1; -;
DR EMBL: Y07250; CA669030.1; ALT_INIT.
DR EMBL: Y11389; CA872218.1; -;
DR EMBL: U81521; AAB39762.1; -;
DR HSSP: P24941; ICRP.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Transferrase, Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 1037 1306 PROTEIN_KINASE.
FT NP_BIND 1043 1051 ATP (BY SIMILARITY).
FT BINDING 1066 1066 ATP (BY SIMILARITY).
FT ACT_SITE 1181 1181 BY SIMILARITY.
FT CONFLICT 484 485 RL -> SP (IN REF. 3).
FT CONFLICT 1346 1346 D -> V (IN REF. 1).
SQ SEQUENCE 1401 AA; 160537 MW; 529A989D2B627F3D CRC64;

Query Match 5.5%; Score 433.5; DB 1; Length 1401;
Best Local Similarity 27.8%; Pred. No. 3e-11;
Matches 119; Conservative 86; Mismatches 162; Indels 61; Gaps 16;

QY 1103 NAVIPSEVTFVPEVKCRDLNVNTELSIEDLLASMPSSDTTTFKSEVAVLSPEKAE 1162
DB 914 NTLILLDDAMFLKIREK-----VKGSMFLL-----TFDVLGAKSKVAA-----KIQ 956
QY 1163 NDTYKDDVNHNNKCKEAEDEEALATAMASASODALPIVPOLOVNGEDIIIIQOD 1222
DB 957 REST---EVSSSPLRFSFGDV-EEALSLQL---LOKETMLRIDELEIBENTLL----- 1004
QY 1223 TPETLP-GHTKAKQPYRE-----DTEWLKGGQIGLGFAPSSCYQADVGTEGL 1268
DB 1005 --ERLAIGHVLDVSFRNRDFIKLASSFSNITIRWQQGHFVRSGMFGDYITGVNMTGDL 1062
QY 1269 MAYQGVYTVRNTSEGEVEVEALREIRMSHLNHNITRMLGATCKEKNYNLFTIEWMAG 1328
DB 1063 LAVKEIKL--QDSRTFRSDVDQHNMVTLRNLNHNVTYTGVEVREKVIYFMEFCQG 1120
QY 1329 GSAVHLISKYGAFKESVIVNTYQLRGLSYLHENOIIHRVKGANLLIDSTGQRURAD 1388
DB 1121 GSLADLLAGRIEDENLVKVVYVQLLEGLAYIHSQHILHRDIKIPANILLDHGM-IKYSD 1179
QY 1389 FGAARLASKGTGAGEFQG-----QLIGTIAPMAPEVLRGQOYG--RSCDVMSVGCALI 1440
DB 1180 FGALVYSPPTDEVRVEDIQPELQHLAGTPMYNAPEIILGKKGDFGAMDIHSLGCVIL 1239
QY 1441 EMACAKPPWNAEKSHNLALIFKIASATTAPSPH--LSPGLRDVALRCLELPQODRPP 1498
DB 1240 EMVTGSTPWS--EMDNWAIYHVAAMHT-PSIPONEKISSIARDPFIQCQFERDPEQRPR 1296
QY 1499 SRELLKHP 1506
DB 1297 AVDLLTHP 1304

RESULT 15
M3K5_HUMAN
ID M3K5_HUMAN STANDARD; PRT; 1374 AA.
AC Q99663; Q99461.
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Mitogen-activated protein kinase kinase kinase 5 (EC 2.7.1.1-)
DE (MAPK/ERK kinase kinase 5) (MEK kinase 5) (MEKK 5) (Apoptosis signal-
DE regulating kinase 1) (ASK-1).
GN MAP3K5 OR MAPKKK5 OR MEKK5 OR ASK1.

OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97034945; PubMed-8940179;
RA Wang X.S., Diener K., Jannuzzi D., Trollinger D., Tan T.-H.,
RA Lichenstein H., Zukowski M., Yao Z.;
RT "Molecular cloning and characterization of a novel protein kinase with
RT a catalytic domain homologous to mitogen-activated protein kinase
RT kinase kinase.";
RL J. Biol. Chem. 271:31607-31611(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-97130104; PubMed-8974401;
RA Ichijo H., Nishida E., Irie K., ten Dijke P., Saitoh M., Moriguchi T.,
RA Takagi M., Matsumoto K., Miyazono K., Gotoh Y.;
RT "Induction of apoptosis by ASK1, a mammalian MAPKKK that activates
RT SAPK/JNK and p38 signaling pathways.";
RL Science 275:90-94(1997).
RN [3]
RP SEQUENCE OF 419-1374 FROM N.A.
RL Phillips S.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PHOSPHORYLATES AND ACTIVATES TWO DIFFERENT SUBGROUPS OF
CC MAP KINASE KINASES, MKK4/SEK1 AND MKK3/MAPKK6 (OR MKK6), WHICH IN
CC TURN ACTIVATED STRESS-ACTIVATED PROTEIN KINASE (SAPK, ALSO KNOWN
CC AS JNK; C-JUN AMINO-TERMINAL KINASE) AND p38 SUBGROUPS OF MAP
CC KINASES, RESPECTIVELY. OVEREXPRESSION INDUCES APOPTOTIC CELL
CC DEATH.
CC -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN HEART AND PANCREAS.
CC -!- INDUCTION: BY TNF-ALPHA.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE SUBFAMILY.
CC -----
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DR EMBL: U67156; AAC50894.1; -;
DR EMBL: D84476; BAA12684.1; -;
DR EMBL: AL024508; CAA19711.1; -;
DR HSSP: Q63450; 1A06.
DR Genew: HGNC:6857; MAP3K5.
DR MIM: 602448; -;
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferrase, Serine/threonine-protein kinase; ATP-binding; Apoptosis.
FT DOMAIN 680 938 PROTEIN_KINASE.
FT NP_BIND 686 693 ATP (BY SIMILARITY).
FT BINDING 709 709 ATP (BY SIMILARITY).
FT ACT_SITE 803 803 BY SIMILARITY.
FT CONFLICT 763 763 S -> Y (IN REF. 2).
FT CONFLICT 959 959 N -> NA (IN REF. 2).
FT CONFLICT 1308 1308 T -> I (IN REF. 2).
SQ SEQUENCE 1374 AA; 154536 MW; 265BDC65986AF985 CRC64;

Query Match 5.5%; Score 430.5; DB 1; Length 1374;
Best Local Similarity 36.6%; Pred. No. 4e-11;
Matches 96; Conservative 48; Mismatches 97; Indels 21; Gaps 7;

